SEQUENCE LISTING

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        Frazer, Ian Hector and Zhou, Jian (US only)
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 gtc cca att ctc gtg gaa ctg gat ggc gat gtg aat ggg cac aaa ttt
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Leu Lys Phe Ile 50	e Cys Thr	Thr Gly 55	Lys Leu	Pro Val 60	Pro Trp	Pro Thr	
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Asp His Met Lys	Gln His 85	Asp Phe	Phe Lys 90	Ser Ala	Met Pro	Glu Gly 95	
Tyr Val Gln Gli 100	Arg Thr	Ile Phe	Phe Lys 105	Asp Asp	Gly Asn 110	Tyr Lys	
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Glu Leu Lys Gly Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His 130

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Lys Gln Lys Asn Gly Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile
Glu Asp Gly Ser Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro
Ile Gly Asp Gly Pro Val Leu Leu Pro Asp Asn His Tyr Leu Ser Thr
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                                                                  96
Val Pro Ile Leu Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe
             20
                                 25
tet gte age gga gag ggt gaa ggt gat gee aca tae gga aag ete aee
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atc Ile	ggc Gly	gac Asp 195	ggc Gly	cct Pro	gtg Val	ctc Leu	ctc Leu 200	cca Pro	gac Asp	aac Asn	cat His	tac Tyr 205	ctg Leu	tcc Ser	acc Thr	624
cag Gln	tct Ser 210	gcc Ala	ctg Leu	tct Ser	aaa Lys	gat Asp 215	ccc Pro	aac Asn	gaa Glu	aag Lys	aga Arg 220	gac Asp	cac His	atg Met	gtc Val	672

720

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Leu Lys Phe Ile Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro	Thr
Leu Val Thr Thr Phe Ser Tyr Gly Val Gln Cys Phe Ser Arg Tyr 65 70 75	Pro 80
Asp His Met Lys Gln His Asp Phe Phe Lys Ser Ala Met Pro Glu 85 90 95	
Tyr Val Gln Glu Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr 100 105 110	Lys
Thr Arg Ala Glu Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg	Ile
Glu Leu Lys Gly Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly 130 140	His
Lys Leu Glu Tyr Asn Tyr Asn Ser His Asn Val Tyr Ile Met Ala 145 150 155	Asp 160
Lys Gln Lys Asn Gly Ile Lys Val Asn Phe Lys Ile Arg His Asn	Ile

Glu Asp Gly Ser Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro 180 Ile Gly Asp Gly Pro Val Leu Leu Pro Asp Asn His Tyr Leu Ser Thr 200 Gln Ser Ala Leu Ser Lys Asp Pro Asn Glu Lys Arg Asp His Met Val 210	
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Į	ac Asp	cat His	atg Met	aag Lys	cag Gln 85	cat His	gac Asp	ttt Phe	ttc Phe	aag Lys 90	agc Ser	gcc Ala	atg Met	ccc Pro	gag Glu 95	ggc Gly	288
ţ	at [yr	gtg Val	cag Gln	gag Glu 100	aga Arg	acc Thr	atc Ile	ttt Phe	ttc Phe 105	aaa Lys	gat Asp	gac Asp	ggg Gly	aac Asn 110	tac Tyr	aag Lys	336
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Leu Val Thr Thr Phe Ser Tyr Gly Val Gln Cys Phe Ser Arg Tyr Pro 65 70 75 80

Asp His Met Lys Gln His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly 85 90 95

Tyr Val Gln Glu Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys 100 105 110

Thr Arg Ala Glu Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile 115 120 125

Glu Leu Lys Gly Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His 130 135 140

Lys Leu Glu Tyr Asn Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp 145 150 155 160

Lys Gln Lys Asn Gly Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile 165 170 175

Glu Asp Gly Ser Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro 180 185 190

Ile Gly Asp 195	Gly Pro	Val Leu	Leu 200	Pro	Asp	Asn	His	Tyr 205	Leu	Ser	Thr	
Gln Ser Ala 210	Leu Ser	Lys Asp 215	Pro	Asn	Glu	Lys	Arg 220	Asp	His	Met	Val	
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ctg gtc act Leu Val Thr 65	acc ttc Thr Phe	tct tat Ser Tyr 70	ggc Gly	gtg Val	cag Gln	tgc Cys 75	ttt Phe	tcc Ser	aga Arg	tac Tyr	cca Pro 80	240

gac Asp	cat His	atg Met	aag Lys	cag Gln 85	cat His	gac Asp	ttt Phe	ttc Phe	aag Lys 90	agc Ser	gcc Ala	atg Met	ccc Pro	gag Glu 95	ggc Gly	288
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cag Gln	tct Ser 210	gcc Ala	ctg Leu	tct Ser	aaa Lys	gat Asp 215	ccc Pro	aac Asn	gaa Glu	aag Lys	aga Arg 220	gac Asp	cac His	atg Met	gtc Val	672
ctg Leu 225	ctg Leu	gag Glu	ttt Phe	gtg Val	acc Thr 230	gct Ala	gct Ala	ggg Gly	atc Ile	aca Thr 235	cat His	ggc Gly	atg Met	gac Asp	gag Glu 240	720
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Leu Lys Phe Ile Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr 50 55 60

Leu Val Thr Thr Phe Ser Tyr Gly Val Gln Cys Phe Ser Arg Tyr Pro 65 70 75 80

Asp His Met Lys Gln His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly 85 90 95

Tyr Val Gln Glu Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys
100 105 110

Thr Arg Ala Glu Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile 115 120 125

Glu Leu Lys Gly Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His 130 135 140

Lys Leu Glu Tyr Asn Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp 145 150 155 160

Lys Gln Lys Asn Gly Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile 165 170 175

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ctg gtc act acc ttc tct tat ggc gtg cag tgc ttt tcc aga tac cca 240 Leu Val Thr Thr Phe Ser Tyr Gly Val Gln Cys Phe Ser Arg Tyr Pro 65 70 75 80)
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		gct Ala 115									384
		aag Lys									432
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Leu Leu Glu Phe Val Thr Ala Ala Gly Ile Thr His Gly Met Asp Glu

225 230 235 240 Leu Tyr Lys														
Leu Tyr Lys														
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Tyr Val Gln	gag aga acc atc t Glu Arg Thr Ile P 100	tt ttc aaa gat gac gg Phe Phe Lys Asp Asp Gl 105	g aac tac aag 336 y Asn Tyr Lys 110											

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					gac Asp											432
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-	tac Tyr	aag Lys	tga													732
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Leu Tyr Lys

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gtc cca att ctc gtg gaa ctg gat ggc gat gtg aat ggg cac aaa ttt
                                                                   96
Val Pro Ile Leu Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe
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Ser Val Ser Gly Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr
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Leu Lys Phe Ile Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr
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Asp His Met Lys Gln His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly
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tat gtg cag gag aga acc atc ttt ttc aaa gat gac ggg aac tac aag
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Tyr Val Gln Glu Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys
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	ctg Leu															480
	caa Gln															528
	gat Asp															576
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	tct Ser 210															672
ctg Leu 225	ctg Leu	gag Glu	ttt Phe	gtg Val	acc Thr 230	gct Ala	gct Ala	ggg Gly	atc Ile	aca Thr 235	cat His	ggc Gly	atg Met	gac Asp	gag Glu 240	720
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Tyr Val Gln Glu Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys 100 105 110

Thr Arg Ala Glu Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile \$115\$ \$120\$ \$125\$

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Lys Leu Glu Tyr Asn Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp 145 150 155 160

Lys Gln Lys Asn Gly Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile 165 170 175

Glu Asp Gly Ser Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro 180 185

Ile Gly Asp Gly Pro Val Leu Leu Pro Asp Asn His Tyr Leu Ser Thr 195 200 205

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	cat His															288
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	ctg Leu 130															432

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Thr	Arg	Ala 115	Glu	Val	Lys	Phe	Glu 120	Gly	Asp	Thr	Leu	Val 125	Asn	Arg	Ile
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Lys	Gln	Lys	Asn	Gly 165	Ile	Lys	Val	Asn	Phe 170	Lys	Ile	Arg	His	Asn 175	Ile
Glu	Asp	Gly	Ser 180	Val	Gln	Leu	Ala	Asp 185	His	Tyr	Gln	Gln	Asn 190	Thr	Pro
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Gln	Ser 210	Ala	Leu	Ser	Lys	Asp 215	Pro	Asn	Glu	Lys	Arg 220	Asp	His	Met	Val
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Glu Leu Lys Gly Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His
Lys Leu Glu Tyr Asn Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp
Lys Gln Lys Asn Gly Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile
Glu Asp Gly Ser Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro
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Gln Ser Ala Leu Ser Lys Asp Pro Asn Glu Lys Arg Asp His Met Val
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Lys Leu Glu Tyr Asn Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp
Lys Gln Lys Asn Gly Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile
Glu Asp Gly Ser Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro
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Gln Ser Ala Leu Ser Lys Asp Pro Asn Glu Lys Arg Asp His Met Val
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Tyr Val Gln	Glu Arg 100	Thr Ile		he Lys 05	Asp A	Asp Gly	Asn '	Tyr	Lys	

Thr Arg Ala Glu Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile 115 120 125

Glu Leu Lys Gly Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His

135

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Lys Leu Glu Tyr Asn Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp
145
Lys Gln Lys Asn Gly Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile
Glu Asp Gly Ser Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro
Ile Gly Asp Gly Pro Val Leu Leu Pro Asp Asn His Tyr Leu Ser Thr
Gln Ser Ala Leu Ser Lys Asp Pro Asn Glu Lys Arg Asp His Met Val
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Leu Leu Glu Phe Val Thr Ala Ala Gly Ile Thr His Gly Met Asp Glu
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Leu Tyr Lys
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<222> (1)..(732)
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Met Asp Asp Asp Asp Ser Lys Gly Glu Glu Leu Phe Thr Gly Val
gtc cca att ctc gtg gaa ctg gat ggc gat gtg aat ggg cac aaa ttt
                                                                  96
Val Pro Ile Leu Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe
                                 25
tet gte age gga gag ggt gaa ggt gat gee aca tae gga aag ete ace
                                                                  144
Ser Val Ser Gly Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr
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		35				40				45			
	aaa Lys 50												192
	gtc Val												240
	cat His												288
	gtg Val	_	 _					_	_			_	336
	cgc Arg												384
	ctg Leu 130	_		_		_	 _						432
	ctg Leu												480
_	caa Gln	_			_	_		_		_			528
	gat Asp												576
	ggc Gly												624
	tct Ser 210												672

ctg ctg gag ttt gtg acc gct gct ggg atc aca cat ggc atg gac gag Leu Leu Glu Phe Val Thr Ala Ala Gly Ile Thr His Gly Met Asp Glu 225 230 235 240	720
ctg tac aag tga Leu Tyr Lys	732
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Ser Val Ser Gly Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr 35 40 45	
Leu Lys Phe Ile Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr 50 55 60	
Leu Val Thr Thr Phe Ser Tyr Gly Val Gln Cys Phe Ser Arg Tyr Pro 65 70 75 80	
Asp His Met Lys Gln His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly 85 90 95	
Tyr Val Gln Glu Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys 100 105 110	
Thr Arg Ala Glu Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile 115 120 125	
Glu Leu Lys Gly Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His 130 135 140	
Lys Leu Glu Tyr Asn Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp 145 150 155 160	

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Lys Gln Lys Asn Gly Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile
Glu Asp Gly Ser Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro
Ile Gly Asp Gly Pro Val Leu Leu Pro Asp Asn His Tyr Leu Ser Thr
Gln Ser Ala Leu Ser Lys Asp Pro Asn Glu Lys Arg Asp His Met Val
                        215
Leu Leu Glu Phe Val Thr Ala Ala Gly Ile Thr His Gly Met Asp Glu
                    230
Leu Tyr Lys
<210> 27
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gtc cca att ctc gtg gaa ctg gat ggc gat gtg aat ggg cac aaa ttt
                                                                   96
Val Pro Ile Leu Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe
             20
                                 25
tet gtc age gga gag ggt gaa ggt gat gec aca tac gga aag etc ace
                                                                   144
Ser Val Ser Gly Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr
                             40
ctg aaa ttc atc tgc acc act gga aag ctc cct gtg cca tgg cca aca
                                                                   192
Leu Lys Phe Ile Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr
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ctg Leu 65	gtc Val	act Thr	acc Thr	ttc Phe	tct Ser 70	tat Tyr	ggc Gly	gtg Val	cag Gln	tgc Cys 75	ttt Phe	tcc Ser	aga Arg	tac Tyr	cca Pro 80	240
gac Asp	cat His	atg Met	aag Lys	cag Gln 85	cat His	gac Asp	ttt Phe	ttc Phe	aag Lys 90	agc Ser	gcc Ala	atg Met	ccc Pro	gag Glu 95	ggc Gly	288
tat Tyr	gtg Val	cag Gln	gag Glu 100	aga Arg	acc Thr	atc Ile	ttt Phe	ttc Phe 105	aaa Lys	gat Asp	gac Asp	G]À aaa	aac Asn 110	tac Tyr	aag Lys	336
acc Thr	cgc Arg	gct Ala 115	gaa Glu	gtc Val	aag Lys	ttc Phe	gaa Glu 120	ggt Gly	gac Asp	acc Thr	ctg Leu	gtg Val 125	aat Asn	aga Arg	atc Ile	384
gag Glu	ctg Leu 130	aag Lys	ggc Gly	att Ile	gac Asp	ttt Phe 135	aag Lys	gag Glu	gat Asp	gga Gly	aac Asn 140	att Ile	ctc Leu	ggc Gly	cac His	432
aag Lys 145	ctg Leu	gaa Glu	tac Tyr	aac Asn	tat Tyr 150	aac Asn	tcc Ser	cac His	aat Asn	gtg Val 155	tac Tyr	atc Ile	atg Met	gcc Ala	gac Asp 160	480
aag Lys	caa Gln	aag Lys	aat Asn	ggc Gly 165	atc Ile	aag Lys	gtc Val	aac Asn	ttc Phe 170	aag Lys	atc Ile	aga Arg	cac His	aac Asn 175	att Ile	528
gag Glu	gat Asp	gga Gly	tcc Ser 180	gtg Val	cag Gln	ctg Leu	gcc Ala	gac Asp 185	cat His	tat Tyr	caa Gln	cag Gln	aac Asn 190	act Thr	cca Pro	576
atc Ile	ggc Gly	gac Asp 195	ggc Gly	cct Pro	gtg Val	ctc Leu	ctc Leu 200	cca Pro	gac Asp	aac Asn	cat His	tac Tyr 205	ctg Leu	tcc Ser	acc Thr	624
cag Gln	tct Ser 210	gcc Ala	ctg Leu	tct Ser	aaa Lys	gat Asp 215	ccc Pro	aac Asn	gaa Glu	aag Lys	aga Arg 220	gac Asp	cac His	atg Met	gtc Val	672
ctg Leu 225	ctg Leu	gag Glu	ttt Phe	gtg Val	acc Thr 230	gct Ala	gct Ala	ggg Gly	atc Ile	aca Thr 235	cat His	ggc Gly	atg Met	gac Asp	gag Glu 240	720

ctg tac aag tga Leu Tyr Lys 732

<210> 28

<211> 243

<212> PRT

<213> Artificial Sequence

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Val Pro Ile Leu Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe 20 25 30

Ser Val Ser Gly Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr 35 40 45

Leu Lys Phe Ile Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr 50 55 60

Leu Val Thr Thr Phe Ser Tyr Gly Val Gln Cys Phe Ser Arg Tyr Pro 65 70 75 80

Asp His Met Lys Gln His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly 85 90 95

Tyr Val Gln Glu Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys
100 105 110

Thr Arg Ala Glu Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile 115 120 125

Glu Leu Lys Gly Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His 130 135 140

Lys Leu Glu Tyr Asn Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp 145 150 155 160

Lys Gln Lys Asn Gly Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile 165 170 175

Glu Asp Gly Ser Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro

			180					185					190			
Ile	Gly	Asp 195	Gly	Pro	Val	Leu	Leu 200	Pro	Asp	Asn	His	Tyr 205	Leu	Ser	Thr	
Gln	Ser 210	Ala	Leu	Ser	Lys	Asp 215	Pro	Asn	Glu	Lys	Arg 220	Asp	His	Met	Val	
Leu 225	Leu	Glu	Phe	Val	Thr 230	Ala	Ala	Gly	Ile	Thr 235	His	Gly	Met	Asp	Glu 240	
Leu	Tyr	Lys														
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	> CI	os l)	(732))												
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gtc Val	cca Pro	att Ile	ctc Leu 20	gtg Val	gaa Glu	ctg Leu	gat Asp	ggc Gly 25	gat Asp	gtg Val	aat Asn	ggg Gly	cac His 30	aaa Lys	ttt Phe	96
tct Ser	gtc Val	agc Ser 35	gga Gly	gag Glu	ggt Gly	gaa Glu	ggt Gly 40	gat Asp	gcc Ala	aca Thr	tac Tyr	gga Gly 45	aag Lys	ctc Leu	acc Thr	144
ctg Leu	aaa Lys 50	ttc Phe	atc Ile	tgc Cys	acc Thr	act Thr 55	gga Gly	aag Lys	ctc Leu	cct Pro	gtg Val 60	cca Pro	tgg Trp	cca Pro	aca Thr	192
ctg Leu	gtc Val	act Thr	acc Thr	ttc Phe	tct Ser	tat Tyr	ggc Gly	gtg Val	cag Gln	tgc Cys	ttt Phe	tcc Ser	aga Arg	tac Tyr	cca Pro	240

65					70					75					80	
gac Asp	cat His	atg Met	aag Lys	cag Gln 85	cat His	gac Asp	ttt Phe	ttc Phe	aag Lys 90	agc Ser	gcc Ala	atg Met	ccc Pro	gag Glu 95	ggc Gly	288
tat Tyr	gtg Val	cag Gln	gag Glu 100	aga Arg	acc Thr	atc Ile	ttt Phe	ttc Phe 105	aaa Lys	gat Asp	gac Asp	ggg Gly	aac Asn 110	tac Tyr	aag Lys	336
acc Thr	cgc Arg	gct Ala 115	gaa Glu	gtc Val	aag Lys	ttc Phe	gaa Glu 120	ggt Gly	gac Asp	acc Thr	ctg Leu	gtg Val 125	aat Asn	aga Arg	atc Ile	384
gag Glu	ctg Leu 130	aag Lys	ggc Gly	att Ile	gac Asp	ttt Phe 135	aag Lys	gag Glu	gat Asp	gga Gly	aac Asn 140	att Ile	ctc Leu	ggc Gly	cac His	432
aag Lys 145	ctg Leu	gaa Glu	tac Tyr	aac Asn	tat Tyr 150	aac Asn	tcc Ser	cac His	aat Asn	gtg Val 155	tac Tyr	atc Ile	atg Met	gcc Ala	gac Asp 160	480
aag Lys	caa Gln	aag Lys	aat Asn	ggc Gly 165	atc Ile	aag Lys	gtc Val	aac Asn	ttc Phe 170	aag Lys	atc Ile	aga Arg	cac His	aac Asn 175	att Ile	528
gag Glu	gat Asp	gga Gly	tcc Ser 180	gtg Val	cag Gln	ctg Leu	gcc Ala	gac Asp 185	cat His	tat Tyr	caa Gln	cag Gln	aac Asn 190	act Thr	cca Pro	576
atc Ile	ggc Gly	gac Asp 195	ggc Gly	cct Pro	gtg Val	ctc Leu	ctc Leu 200	cca Pro	gac Asp	aac Asn	cat His	tac Tyr 205	ctg Leu	tcc Ser	acc Thr	624
cag Gln	tct Ser 210	gcc Ala	ctg Leu	tct Ser	aaa Lys	gat Asp 215	ccc Pro	aac Asn	gaa Glu	aag Lys	aga Arg 220	gac Asp	cac His	atg Met	gtc Val	672
ctg Leu 225	ctg Leu	gag Glu	ttt Phe	gtg Val	acc Thr 230	gct Ala	gct Ala	Gly ggg	atc Ile	aca Thr 235	cat His	ggc Gly	atg Met	gac Asp	gag Glu 240	720
	tac Tyr	aag Lys	tga													732

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- <211> 243
- <212> PRT
- <213> Artificial Sequence

<400> 30

Met Cys Cys Cys Cys Ser Lys Gly Glu Glu Leu Phe Thr Gly Val 1 5 15

Val Pro Ile Leu Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe 20 25 30

Ser Val Ser Gly Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr 35 40 45

Leu Lys Phe Ile Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr 50 55 60

Leu Val Thr Thr Phe Ser Tyr Gly Val Gln Cys Phe Ser Arg Tyr Pro
65 70 75 80

Asp His Met Lys Gln His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly 85 90 95

Tyr Val Gln Glu Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys
100 105 110

Thr Arg Ala Glu Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile 115 120 125

Glu Leu Lys Gly Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His 130 135 140

Lys Leu Glu Tyr Asn Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp 145 150 155 160

Lys Gln Lys Asn Gly Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile 165 170 175

Glu Asp Gly Ser Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro 180 185 190

Ile Gly Asp Gly Pro Val Leu Leu Pro Asp Asn His Tyr Leu Ser Thr 195 200 205

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Gln Ser Ala Leu Ser Lys Asp Pro Asn Glu Lys Arg Asp His Met Val
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Leu Leu Glu Phe Val Thr Ala Ala Gly Ile Thr His Gly Met Asp Glu
225
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Leu Tyr Lys
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gtc cca att ctc gtg gaa ctg gat ggc gat gtg aat ggg cac aaa ttt
                                                                   96
Val Pro Ile Leu Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe
tet gte age gga gag ggt gaa ggt gat gee aca tae gga aag ete ace
                                                                   144
Ser Val Ser Gly Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr
                             40
ctg aaa ttc atc tgc acc act gga aag ctc cct gtg cca tgg cca aca
                                                                   192
Leu Lys Phe Ile Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr
                                             60
ctg gtc act acc ttc tct tat ggc gtg cag tgc ttt tcc aga tac cca
                                                                   240
Leu Val Thr Thr Phe Ser Tyr Gly Val Gln Cys Phe Ser Arg Tyr Pro
gac cat atg aag cag cat gac ttt ttc aag agc gcc atg ccc gag ggc
                                                                   288
Asp His Met Lys Gln His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly
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				85					90					95		
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acc Thr	cgc Arg	gct Ala 115	gaa Glu	gtc Val	aag Lys	ttc Phe	gaa Glu 120	ggt Gly	gac Asp	acc Thr	ctg Leu	gtg Val 125	aat Asn	aga Arg	atc Ile	384
gag Glu	ctg Leu 130	aag Lys	ggc Gly	att Ile	gac Asp	ttt Phe 135	aag Lys	gag Glu	gat Asp	gga Gly	aac Asn 140	att Ile	ctc Leu	ggc Gly	cac His	432
aag Lys 145	ctg Leu	gaa Glu	tac Tyr	aac Asn	tat Tyr 150	aac Asn	tcc Ser	cac His	aat Asn	gtg Val 155	tac Tyr	atc Ile	atg Met	gcc Ala	gac Asp 160	480
aag Lys	caa Gln	aag Lys	aat Asn	ggc Gly 165	atc Ile	aag Lys	gtc Val	aac Asn	ttc Phe 170	aag Lys	atc Ile	aga Arg	cac His	aac Asn 175	att Ile	528
gag Glu	gat Asp	gga Gly	tcc Ser 180	gtg Val	cag Gln	ctg Leu	gcc Ala	gac Asp 185	cat His	tat Tyr	caa Gln	cag Gln	aac Asn 190	act Thr	cca Pro	576
atc Ile	ggc Gly	gac Asp 195	ggc Gly	cct Pro	gtg Val	ctc Leu	ctc Leu 200	cca Pro	gac Asp	aac Asn	cat His	tac Tyr 205	ctg Leu	tcc Ser	acc Thr	624
cag Gln	tct Ser 210	gcc Ala	ctg Leu	tct Ser	aaa Lys	gat Asp 215	ccc Pro	aac Asn	gaa Glu	aag Lys	aga Arg 220	gac Asp	cac His	atg Met	gtc Val	672
ctg Leu 225	ctg Leu	gag Glu	ttt Phe	gtg Val	acc Thr 230	gct Ala	gct Ala	ggg Gly	atc Ile	aca Thr 235	cat His	ggc Gly	atg Met	gac Asp	gag Glu 240	720
_	tac Tyr	aag Lys	tga													732
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<211> 243 <212> PRT

<213> Artificial Sequence

<400> 32

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Val Pro Ile Leu Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe 20 25 30

Ser Val Ser Gly Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr 35 40 45

Leu Lys Phe Ile Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr 50 55 60

Leu Val Thr Thr Phe Ser Tyr Gly Val Gln Cys Phe Ser Arg Tyr Pro 65 70 75 80

Asp His Met Lys Gln His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly 85 90 95

Tyr Val Gln Glu Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys
100 105 110

Thr Arg Ala Glu Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile 115 120 125

Glu Leu Lys Gly Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His 130 135 140

Lys Leu Glu Tyr Asn Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp 145 150 155 160

Lys Gln Lys Asn Gly Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile 165 170 175

Glu Asp Gly Ser Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro 180 185

Ile Gly Asp Gly Pro Val Leu Leu Pro Asp Asn His Tyr Leu Ser Thr 195 200 205

Gln Ser Ala Leu Ser Lys Asp Pro Asn Glu Lys Arg Asp His Met Val 210 215 220

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Leu	Tyr	Lys														
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)> 3:															
Met 1	Gln	Gln	Gln	caa Gln 5	Gln	agc Ser	aag Lys	Gly	gag Glu 10	gaa Glu	ctg Leu	ttc Phe	act Thr	ggc Gly 15	gtg Val	48
gtc Val	cca Pro	att Ile	ctc Leu 20	gtg Val	gaa Glu	ctg Leu	gat Asp	ggc Gly 25	gat Asp	gtg Val	aat Asn	Glà aaa	cac His 30	aaa Lys	ttt Phe	96
tct Ser	gtc Val	agc Ser 35	gga Gly	gag Glu	ggt Gly	gaa Glu	ggt Gly 40	gat Asp	gcc Ala	aca Thr	tac Tyr	gga Gly 45	aag Lys	ctc Leu	acc Thr	144
ctg Leu	aaa Lys 50	ttc Phe	atc Ile	tgc Cys	acc Thr	act Thr 55	gga Gly	aag Lys	ctc Leu	cct Pro	gtg Val 60	cca Pro	tgg Trp	cca Pro	aca Thr	192
ctg Leu 65	gtc Val	act Thr	acc Thr	ttc Phe	tct Ser 70	tat Tyr	ggc Gly	gtg Val	cag Gln	tgc Cys 75	ttt Phe	tcc Ser	aga Arg	tac Tyr	cca Pro 80	240
gac Asp	cat His	atg Met	aag Lys	cag Gln 85	cat His	gac Asp	ttt Phe	ttc Phe	aag Lys 90	agc Ser	gcc Ala	atg Met	ccc Pro	gag Glu 95	ggc Gly	288
tat Tyr	gtg Val	cag Gln	gag Glu	aga Arg	acc Thr	atc Ile	ttt Phe	ttc Phe	aaa Lys	gat Asp	gac Asp	ggg Gly	aac Asn	tac Tyr	aag Lys	336

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acc cgc gct Thr Arg Ala 115	gaa gtc aac Glu Val Lys	ttc gaa gg Phe Glu Gl 120	t gac acc ctg gt y Asp Thr Leu Va 12	l Asn Arg Ile	384
gag ctg aag Glu Leu Lys 130	ggc att gad Gly Ile Asp	ttt aag ga Phe Lys Gl 135	g gat gga aac at u Asp Gly Asn Il 140	t ctc ggc cac e Leu Gly His	432
aag ctg gaa Lys Leu Glu 145	tac aac tat Tyr Asn Tyr 150	Asn Ser Hi	c aat gtg tac at s Asn Val Tyr Il 155	c atg gcc gac e Met Ala Asp 160	480
aag caa aag Lys Gln Lys	aat ggc atc Asn Gly Ile 165	aag gtc aa Lys Val As	c ttc aag atc ag n Phe Lys Ile Ar 170	a cac aac att g His Asn Ile 175	528
gag gat gga Glu Asp Gly	tcc gtg cag Ser Val Glr 180	ctg gcc ga Leu Ala As _j 18	c cat tat caa ca p His Tyr Gln Gl: 5	g aac act cca n Asn Thr Pro 190	576
atc ggc gac Ile Gly Asp 195	ggc cct gtg Gly Pro Val	ctc ctc cc Leu Leu Pro 200	a gac aac cat ta o Asp Asn His Ty 20	r Leu Ser Thr	624
cag tct gcc Gln Ser Ala 210	ctg tct aaa Leu Ser Lys	gat ccc aa Asp Pro As 215	c gaa aag aga ga n Glu Lys Arg As _] 220	c cac atg gtc p His Met Val	672
ctg ctg gag Leu Leu Glu 225	ttt gtg acc Phe Val Thr 230	gct gct ggo Ala Ala Gl	g atc aca cat ggg y Ile Thr His Gl 235	c atg gac gag y Met Asp Glu 240	720
ctg tac aag Leu Tyr Lys	tga				732
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<212> PRT <213> Artificial Sequence

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Ser	Val	Ser 35	Gly	Glu	Gly	Glu	Gly 40	Asp	Ala	Thr	Tyr	Gly 45	Lys	Leu	Thr
Leu	Lys 50	Phe	Ile	Cys	Thr	Thr 55	Gly	Lys	Leu	Pro	Val 60	Pro	Trp	Pro	Thr
Leu 65	Val	Thr	Thr	Phe	Ser 70	Tyr	Gly	Val	Gln	Cys 75	Phe	Ser	Arg	Tyr	Pro 80
Asp	His	Met	Lys	Gln 85	His	Asp	Phe	Phe	Lys 90	Ser	Ala	Met	Pro	Glu 95	Gly
Tyr	Val	Gln	Glu 100	Arg	Thr	Ile	Phe	Phe 105	Lys	Asp	Asp	Gly	Asn 110	Tyr	Lys
Thr	Arg	Ala 115	Glu	Val	Lys	Phe	Glu 120	Gly	Asp	Thr	Leu	Val 125	Asn	Arg	Ile
Glu	Leu 130	Lys	Gly	Ile	Asp	Phe 135	Lys	Glu	Asp	Gly	Asn 140	Ile	Leu	Gly	His
Lys 145	Leu	Glu	Tyr	Asn	Tyr 150	Asn	Ser	His	Asn	Val 155	Tyr	Ile	Met	Ala	Asp 160
Lys	Gln	Lys	Asn	Gly 165	Ile	Lys	Val	Asn	Phe 170	Lys	Ile	Arg	His	Asn 175	Ile
Glu	Asp	Gly	Ser 180	Val	Gln	Leu	Ala	Asp 185	His	Tyr	Gln	Gln	Asn 190	Thr	Pro
Ile	Gly	Asp 195	Gly	Pro	Val	Leu	Leu 200	Pro	Asp	Asn	His	Tyr 205	Leu	Ser	Thr
Gln	Ser 210	Ala	Leu	Ser	Lys	Asp 215	Pro	Asn	Glu	Lys	Arg 220	Asp	His	Met	Val
Leu 225	Leu	Glu	Phe	Val	Thr 230	Ala	Ala	Gly	Ile	Thr 235	His	Gly	Met	Asp	Glu 240
Leu	Tyr	Lys													

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gtc cca att ctc gtg gaa ctg gat ggc gat gtg aat ggg cac aaa ttt
                                                                   96
Val Pro Ile Leu Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe
tet gte age gga gag ggt gaa ggt gat gee aca tae gga aag ete ace
                                                                   144
Ser Val Ser Gly Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr
         35
                             40
ctg aaa ttc atc tgc acc act gga aag ctc cct gtg cca tgg cca aca
                                                                   192
Leu Lys Phe Ile Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr
ctg gtc act acc ttc tct tat ggc gtg cag tgc ttt tcc aga tac cca
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Leu Val Thr Thr Phe Ser Tyr Gly Val Gln Cys Phe Ser Arg Tyr Pro
gac cat atg aag cag cat gac ttt ttc aag agc gcc atg ccc gag ggc
                                                                   288
Asp His Met Lys Gln His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly
                 85
tat gtg cag gag aga acc atc ttt ttc aaa gat gac ggg aac tac aag
                                                                   336
Tyr Val Gln Glu Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys
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                                                    110
acc cgc gct gaa gtc aag ttc gaa ggt gac acc ctg gtg aat aga atc
                                                                   384
Thr Arg Ala Glu Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile
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		115					120					125				
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		aag Lys														528
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		gac Asp 195														624
cag Gln	tct Ser 210	gcc Ala	ctg Leu	tct Ser	aaa Lys	gat Asp 215	ccc Pro	aac Asn	gaa Glu	aag Lys	aga Arg 220	gac Asp	cac His	atg Met	gtc Val	672
ctg Leu 225	ctg Leu	gag Glu	ttt Phe	gtg Val	acc Thr 230	gct Ala	gct Ala	ggg Gly	atc Ile	aca Thr 235	cat His	ggc Gly	atg Met	gac Asp	gag Glu 240	720
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Ser Val Ser Gly Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr Phe Ser Tyr Gly Val Gln Cys Phe Ser Arg Tyr Pro Asp His Met Lys Gln His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr Asn Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp Lys Gln Lys Asn Gly Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile Glu Asp Gly Ser Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro 180 185 Ile Gly Asp Gly Pro Val Leu Leu Pro Asp Asn His Tyr Leu Ser Thr 195 200 205 Gln Ser Ala Leu Ser Lys Asp Pro Asn Glu Lys Arg Asp His Met Val 215 Leu Leu Glu Phe Val Thr Ala Ala Gly Ile Thr His Gly Met Asp Glu

230

Leu Tyr Lys

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235

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Val Pro Ile Leu Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe
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Ser Val Ser Gly Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr
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Leu Lys Phe Ile Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr
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ctg gtc act acc ttc tct tat ggc gtg cag tgc ttt tcc aga tac cca
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Leu Val Thr Thr Phe Ser Tyr Gly Val Gln Cys Phe Ser Arg Tyr Pro
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                                         75
gac cat atg aag cag cat gac ttt ttc aag agc gcc atg ccc gag ggc
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Asp His Met Lys Gln His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly
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tat gtg cag gag aga acc atc ttt ttc aaa gat gac ggg aac tac aag
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Tyr Val Gln Glu Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys
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                                105
acc ege get gaa gte aag tte gaa ggt gae acc etg gtg aat aga atc
                                                                   384
Thr Arg Ala Glu Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile
                            120
                                                 125
gag ctg aag ggc att gac ttt aag gag gat gga aac att ctc ggc cac
                                                                   432
Glu Leu Lys Gly Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His
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gag Glu	gat Asp	gga Gly	tcc Ser 180	gtg Val	cag Gln	ctg Leu	gcc Ala	gac Asp 185	cat His	tat Tyr	caa Gln	cag Gln	aac Asn 190	act Thr	cca Pro	576
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cag Gln	tct Ser 210	gcc Ala	ctg Leu	tct Ser	aaa Lys	gat Asp 215	ccc Pro	aac Asn	gaa Glu	aag Lys	aga Arg 220	gac Asp	cac His	atg Met	gtc Val	672
ctg Leu 225	ctg Leu	gag Glu	ttt Phe	gtg Val	acc Thr 230	gct Ala	gct Ala	ggg	atc Ile	aca Thr 235	cat His	ggc Gly	atg Met	gac Asp	gag Glu 240	720
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Val	Pro	Ile	Leu 20	Val	Glu	Leu	Asp	Gly 25	Asp	Val	Asn	Gly	His 30	Lys	Phe	
Ser	Val	Ser 35	Gly	Glu	Gly	Glu	Gly 40	Asp	Ala	Thr	Tyr	Gly 45	Lys	Leu	Thr	

Leu Lys Phe Ile Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr 50 60

Leu Val Thr Thr Phe Ser Tyr Gly Val Gln Cys Phe Ser Arg Tyr Pro 65 70 75 80

Asp His Met Lys Gln His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly $85 \hspace{1.5cm} 90 \hspace{1.5cm} 95$

Tyr Val Glu Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys
100 105

Thr Arg Ala Glu Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile 115 120 125

Glu Leu Lys Gly Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His 130 135 140

Lys Leu Glu Tyr Asn Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp 145 150 155 160

Lys Gln Lys Asn Gly Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile
165 170 175

Glu Asp Gly Ser Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro $180 \hspace{1cm} 185 \hspace{1cm} 190 \hspace{1cm}$

Ile Gly Asp Gly Pro Val Leu Leu Pro Asp Asn His Tyr Leu Ser Thr 195 200 205

Gln Ser Ala Leu Ser Lys Asp Pro Asn Glu Lys Arg Asp His Met Val $210 \\ 215 \\ 220$

Leu Leu Glu Phe Val Thr Ala Ala Gly Ile Thr His Gly Met Asp Glu 225 230 235 240

Leu Tyr Lys

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Lys Leu Glu Tyr Asn Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp

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gag Glu	gat Asp	gga Gly	tcc Ser 180	gtg Val	cag Gln	ctg Leu	gcc Ala	gac Asp 185	cat His	tat Tyr	caa Gln	cag Gln	aac Asn 190	act Thr	cca Pro	576
atc Ile	ggc Gly	gac Asp 195	ggc Gly	cct Pro	gtg Val	ctc Leu	ctc Leu 200	cca Pro	gac Asp	aac Asn	cat His	tac Tyr 205	ctg Leu	tcc Ser	acc Thr	624
cag Gln	tct Ser 210	gcc Ala	ctg Leu	tct Ser	aaa Lys	gat Asp 215	ccc Pro	aac Asn	gaa Glu	aag Lys	aga Arg 220	gac Asp	cac His	atg Met	gtc Val	672
ctg Leu 225	ctg Leu	gag Glu	ttt Phe	gtg Val	acc Thr 230	gct Ala	gct Ala	ggg Gly	atc Ile	aca Thr 235	cat His	ggc Gly	atg Met	gac Asp	gag Glu 240	720
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Ser	Val	Ser 35	Gly	Glu	Gly	Glu	Gly 40	Asp	Ala	Thr	Tyr	Gly 45	Lys	Leu	Thr	
Leu	Lys 50	Phe	Ile	Cys	Thr	Thr 55	Gly	Lys	Leu	Pro	Val 60	Pro	Trp	Pro	Thr	
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Tyr	Val	Gln	Glu 100	Arg	Thr	Ile	Phe	Phe 105	Lys	Asp	Asp	Gly	Asn 110	Tyr	Lys
Thr	Arg	Ala 115	Glu	Val	Lys	Phe	Glu 120	Gly	Asp	Thr	Leu	Val 125	Asn	Arg	Ile
Glu	Leu 130	Lys	Gly	Ile	Asp	Phe 135	Lys	Glu	Asp	Gly	Asn 140	Ile	Leu	Gly	His
Lys 145	Leu	Glu	Tyr	Asn	Tyr 150	Asn	Ser	His	Asn	Val 155	Tyr	Ile	Met	Ala	Asp 160
Lys	Gln	Lys	Asn	Gly 165	Ile	Lys	Val	Asn	Phe 170	Lys	Ile	Arg	His	Asn 175	Ile
Glu	Asp	Gly	Ser 180	Val	Gln	Leu	Ala	Asp 185	His	Tyr	Gln	Gln	Asn 190	Thr	Pro
Ile	Gly	Asp 195	Gly	Pro	Val	Leu	Leu 200	Pro	Asp	Asn	His	Tyr 205	Leu	Ser	Thr
Gln	Ser 210	Ala	Leu	Ser	Lys	Asp 215	Pro	Asn	Glu	Lys	Arg 220	Asp	His	Met	Val
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t	ct Ser	gtc Val	agc Ser 35	gga Gly	gag Glu	ggt Gly	gaa Glu	ggt Gly 40	gat Asp	gcc Ala	aca Thr	tac Tyr	gga Gly 45	aag Lys	ctc Leu	acc Thr	144
I	tg Leu	aaa Lys 50	ttc Phe	atc Ile	tgc Cys	acc Thr	act Thr 55	gga Gly	aag Lys	ctc Leu	cct Pro	gtg Val 60	cca Pro	tgg Trp	cca Pro	aca Thr	192
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t	at 'yr	gtg Val	cag Gln	gag Glu 100	aga Arg	acc Thr	atc Ile	ttt Phe	ttc Phe 105	aaa Lys	gat Asp	gac Asp	ggg Gly	aac Asn 110	tac Tyr	aag Lys	336
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9	ag Slu	ctg Leu 130	aag Lys	ggc Gly	att Ile	gac Asp	ttt Phe 135	aag Lys	gag Glu	gat Asp	gga Gly	aac Asn 140	att Ile	ctc Leu	ggc Gly	cac His	432
I	ag ys 45	ctg Leu	gaa Glu	tac Tyr	aac Asn	tat Tyr 150	aac Asn	tcc Ser	cac His	aat Asn	gtg Val 155	tac Tyr	atc Ile	atg Met	gcc Ala	gac Asp 160	480
ā	ag ys	caa Gln	aag Lys	aat Asn	ggc Gly	atc Ile	aag Lys	gtc Val	aac Asn	ttc Phe	aag Lys	atc Ile	aga Arg	cac His	aac Asn	att Ile	528

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cag tot gcc ctg tot Gln Ser Ala Leu Ser 210			
ctg ctg gag ttt gtg Leu Leu Glu Phe Val 225	acc gct gct ggg Thr Ala Ala Gly 230	atc aca cat ggc Ile Thr His Gly 235	atg gac gag 720 Met Asp Glu 240
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Leu Lys Phe Ile Cys 50	Thr Thr Gly Lys	Leu Pro Val Pro 60	Trp Pro Thr
Leu Val Thr Thr Phe	Com Mira Clar Mal	-	
65	70	Gln Cys Phe Ser 75	Arg Tyr Pro 80

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Glu Leu Lys Gly Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His
Lys Leu Glu Tyr Asn Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp
Lys Gln Lys Asn Gly Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile
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Glu Asp Gly Ser Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro
Ile Gly Asp Gly Pro Val Leu Leu Pro Asp Asn His Tyr Leu Ser Thr
        195
Gln Ser Ala Leu Ser Lys Asp Pro Asn Glu Lys Arg Asp His Met Val
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tct Ser	gtc Val	agc Ser 35	gga Gly	gag Glu	ggt Gly	gaa Glu	ggt Gly 40	gat Asp	gcc Ala	aca Thr	tac Tyr	gga Gly 45	aag Lys	ctc Leu	acc Thr	144
							gga Gly									192
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gag Glu	gat Asp	gga Gly	tcc Ser	gtg Val	cag Gln	ctg Leu	gcc Ala	gac Asp	cat His	tat Tyr	caa Gln	cag Gln	aac Asn	act Thr	cca Pro	576

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cag tot gcc Gln Ser Ala 210	ctg tct Leu Ser	aaa gat Lys Asp 215	Pro	aac Asn	gaa Glu	aag Lys	aga Arg 220	gac Asp	cac His	atg Met	gtc Val	672
ctg ctg gag Leu Leu Glu 225	ttt gtg Phe Val	acc gct Thr Ala 230	gct Ala	gly	atc Ile	aca Thr 235	cat His	ggc Gly	atg Met	gac Asp	gag Glu 240	720
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Val Pro Ile Ser Val Ser 35 Leu Lys Phe	Leu Val 20 Gly Glu Ile Cys	Glu Leu Gly Glu Thr Thr 55	Asp Gly 40 Gly	Gly 25 Asp Lys	10 Asp Ala Leu	Val Thr Pro	Asn Tyr Val 60	Gly Gly 45 Pro	His 30 Lys Trp	15 Lys Leu Pro	Phe Thr	
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Lys Gln Lys Asn Gly Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile
Glu Asp Gly Ser Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro
Ile Gly Asp Gly Pro Val Leu Leu Pro Asp Asn His Tyr Leu Ser Thr
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96

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tat Tyr	gtg Val	cag Gln	gag Glu 100	aga Arg	acc Thr	atc Ile	ttt Phe	ttc Phe 105	aaa Lys	gat Asp	gac Asp	Gly ggg	aac Asn 110	tac Tyr	aag Lys	336
acc Thr	cgc Arg	gct Ala 115	gaa Glu	gtc Val	aag Lys	ttc Phe	gaa Glu 120	ggt Gly	gac Asp	acc Thr	ctg Leu	gtg Val 125	aat Asn	aga Arg	atc Ile	384
gag Glu	ctg Leu 130	aag Lys	ggc Gly	att Ile	gac Asp	ttt Phe 135	aag Lys	gag Glu	gat Asp	gga Gly	aac Asn 140	att Ile	ctc Leu	ggc	cac His	432
aag Lys 145	ctg Leu	gaa Glu	tac Tyr	aac Asn	tat Tyr 150	aac Asn	tcc Ser	cac His	aat Asn	gtg Val 155	tac Tyr	atc Ile	atg Met	gcc Ala	gac Asp 160	480
aag Lys	caa Gln	aag Lys	aat Asn	ggc Gly 165	atc Ile	aag Lys	gtc Val	aac Asn	ttc Phe 170	aag Lys	atc Ile	aga Arg	cac His	aac Asn 175	att Ile	528
gag Glu	gat Asp	gga Gly	tcc Ser 180	gtg Val	cag Gln	ctg Leu	gcc Ala	gac Asp 185	cat His	tat Tyr	caa Gln	cag Gln	aac Asn 190	act Thr	cca Pro	576
atc Ile	ggc Gly	gac Asp	ggc Gly	cct Pro	gtg Val	ctc Leu	ctc Leu	cca Pro	gac Asp	aac Asn	cat His	tac Tyr	ctg Leu	tcc Ser	acc Thr	624

195	200	205	
cag tot goo otg to Gln Ser Ala Leu Se 210	t aaa gat ccc aac r Lys Asp Pro Asn 215	gaa aag aga gac Glu Lys Arg Asp 220	cac atg gtc 672 His Met Val
ctg ctg gag ttt gt	g acc gct gct ggg	atc aca cat ggc	atg gac gag 720
Leu Leu Glu Phe Va	1 Thr Ala Ala Gly	Ile Thr His Gly	Met Asp Glu
225	230	235	240
ctg tac aag tga Leu Tyr Lys			732
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Val Pro Ile Leu Va	l Glu Leu Asp Gly	Asp Val Asn Gly	His Lys Phe
20	25		30
Ser Val Ser Gly Gl	u Gly Glu Gly Asp	Ala Thr Tyr Gly	Lys Leu Thr
35	40	45	
Leu Lys Phe Ile Cy	s Thr Thr Gly Lys	Leu Pro Val Pro	Trp Pro Thr
50	55	60	
Leu Val Thr Thr Ph	e Ser Tyr Gly Val	Gln Cys Phe Ser	Arg Tyr Pro
65	70	75	80
Asp His Met Lys Gl		Lys Ser Ala Met	Pro Glu Gly
8		90	95
Tyr Val Gln Glu Ar	g Thr Ile Phe Phe	Lys Asp Asp Gly	Asn Tyr Lys
100	105		110
Thr Arg Ala Glu Va 115	l Lys Phe Glu Gly 120	Asp Thr Leu Val	Asn Arg Ile
Glu Leu Lys Gly Il	e Asp Phe Lys Glu	Asp Gly Asn Ile	Leu Gly His

	130					135					140					
Lys 145	Leu	Glu	Tyr	Asn	Tyr 150	Asn	Ser	His	Asn	Val 155	Tyr	Ile	Met	Ala	Asp 160	
Lys	Gln	Lys	Asn	Gly 165	Ile	Lys	Val	Asn	Phe 170	Lys	Ile	Arg	His	Asn 175	Ile	
Glu	Asp	Gly	Ser 180	Val	Gln	Leu	Ala	Asp 185	His	Tyr	Gln	Gln	Asn 190	Thr	Pro	
Ile	Gly	Asp 195	Gly	Pro	Val	Leu	Leu 200	Pro	Asp	Asn	His	Tyr 205	Leu	Ser	Thr	
Gln	Ser 210	Ala	Leu	Ser	Lys	Asp 215	Pro	Asn	Glu	Lys	Arg 220	Asp	His	Met	Val	
Leu 225	Leu	Glu	Phe	Val	Thr 230	Ala	Ala	Gly	Ile	Thr 235	His	Gly	Met	Asp	Glu 240	
Leu	Tyr	Lys														
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)> 1> CI 2> (1		(732)													
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gtc Val	cca Pro	att Ile	ctc Leu 20	gtg Val	gaa Glu	ctg Leu	gat Asp	ggc Gly 25	gat Asp	gtg Val	aat Asn	ggg Gly	cac His 30	aaa Lys	ttt Phe	96
tct	gtc	agc	gga	gag	ggt	gaa	ggt	gat	gcc	aca	tac	gga	aag	ctc	acc	144

Ser	Val	Ser 35	Gly	Glu	Gly	Glu	Gly 40	Asp	Ala	Thr	Tyr	Gly 45	Lys	Leu	Thr	
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ctg Leu 65	gtc Val	act Thr	acc Thr	ttc Phe	tct Ser 70	tat Tyr	ggc Gly	gtg Val	cag Gln	tgc Cys 75	ttt Phe	tcc Ser	aga Arg	tac Tyr	cca Pro 80	240
gac Asp	cat His	atg Met	aag Lys	cag Gln 85	cat His	gac Asp	ttt Phe	ttc Phe	aag Lys 90	agc Ser	gcc Ala	atg Met	ccc Pro	gag Glu 95	ggc Gly	288
tat Tyr	gtg Val	cag Gln	gag Glu 100	aga Arg	acc Thr	atc Ile	ttt Phe	ttc Phe 105	aaa Lys	gat Asp	gac Asp	Gly ggg	aac Asn 110	tac Tyr	aag Lys	336
acc Thr	cgc Arg	gct Ala 115	gaa Glu	gtc Val	aag Lys	ttc Phe	gaa Glu 120	ggt Gly	gac Asp	acc Thr	ctg Leu	gtg Val 125	aat Asn	aga Arg	atc Ile	384
gag Glu	ctg Leu 130	aag Lys	ggc Gly	att Ile	gac Asp	ttt Phe 135	aag Lys	gag Glu	gat Asp	gga Gly	aac Asn 140	att Ile	ctc Leu	ggc Gly	cac His	432
aag Lys 145	ctg Leu	gaa Glu	tac Tyr	aac Asn	tat Tyr 150	aac Asn	tcc Ser	cac His	aat Asn	gtg Val 155	tac Tyr	atc Ile	atg Met	gcc Ala	gac Asp 160	480
aag Lys	caa Gln	aag Lys	aat Asn	ggc Gly 165	atc Ile	aag Lys	gtc Val	aac Asn	ttc Phe 170	aag Lys	atc Ile	aga Arg	cac His	aac Asn 175	att Ile	528
gag Glu	gat Asp	gga Gly	tcc Ser 180	gtg Val	cag Gln	ctg Leu	gcc Ala	gac Asp 185	cat His	tat Tyr	caa Gln	cag Gln	aac Asn 190	act Thr	cca Pro	576
atc Ile	ggc Gly	gac Asp 195	ggc Gly	cct Pro	gtg Val	ctc Leu	ctc Leu 200	cca Pro	gac Asp	aac Asn	cat His	tac Tyr 205	ctg Leu	tcc Ser	acc Thr	624
cag Gln	tct Ser	gcc Ala	ctg Leu	tct Ser	aaa Lys	gat Asp	ccc Pro	aac Asn	gaa Glu	aag Lys	aga Arg	gac Asp	cac His	atg Met	gtc Val	672

210 215 220 ctg ctg gag ttt gtg acc gct gct ggg atc aca cat ggc atg gac gag 720 Leu Leu Glu Phe Val Thr Ala Ala Gly Ile Thr His Gly Met Asp Glu 225 230 ctg tac aag tga 732 Leu Tyr Lys <210> 48 <211> 243 <212> PRT <213> Artificial Sequence <400> 48 Met Gly Gly Gly Gly Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe 20 Ser Val Ser Gly Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr 55 Leu Val Thr Thr Phe Ser Tyr Gly Val Gln Cys Phe Ser Arg Tyr Pro Asp His Met Lys Gln His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys 105 Thr Arg Ala Glu Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His 135 Lys Leu Glu Tyr Asn Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp 150 155

гуѕ	GIN	ьуs	ASN	165	iie	гàг	va⊥	Asn	170	ьys	ile	Arg	HlS	175	TIE	
Glu	Asp	Gly	Ser 180	Val	Gln	Leu	Ala	Asp 185	His	Tyr	Gln	Gln	Asn 190	Thr	Pro	
Ile	Gly	Asp 195	Gly	Pro	Val	Leu	Leu 200	Pro	Asp	Asn	His	Tyr 205	Leu	Ser	Thr	
Gln	Ser 210	Ala	Leu	Ser	Lys	Asp 215	Pro	Asn	Glu	Lys	Arg 220	Asp	His	Met	Val	
Leu 225	Leu	Glu	Phe	Val	Thr 230	Ala	Ala	Gly	Ile	Thr 235	His	Gly	Met	Asp	Glu 240	
Leu	Tyr	Lys														
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<220 <221 <222	.> CI		(732)	ŧ												
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gtc Val	cca Pro	att Ile	ctc Leu 20	gtg Val	gaa Glu	ctg Leu	gat Asp	ggc Gly 25	gat Asp	gtg Val	aat Asn	ggg Gly	cac His 30	aaa Lys	ttt Phe	96
tct Ser	gtc Val	agc Ser 35	gga Gly	gag Glu	ggt Gly	gaa Glu	ggt Gly 40	gat Asp	gcc Ala	aca Thr	tac Tyr	gga Gly 45	aag Lys	ctc Leu	acc Thr	144
ctg	aaa	ttc	atc	tgc	acc	act	gga	aag	ctc	cct	gtg	сса	tgg	сса	aca	192

Leu	Lys 50	Phe	Ile	Cys	Thr	Thr 55	Gly	Lys	Leu	Pro	Val 60	Pro	Trp	Pro	Thr	
	gtc Val															240
	cat His															288
	gtg Val															336
acc Thr	cgc Arg	gct Ala 115	gaa Glu	gtc Val	aag Lys	ttc Phe	gaa Glu 120	ggt Gly	gac Asp	acc Thr	ctg Leu	gtg Val 125	aat Asn	aga Arg	atc Ile	384
	ctg Leu 130															432
aag Lys 145	ctg Leu	gaa Glu	tac Tyr	aac Asn	tat Tyr 150	aac Asn	tcc Ser	cac His	aat Asn	gtg Val 155	tac Tyr	atc Ile	atg Met	gcc Ala	gac Asp 160	480
	caa Gln															528
	gat Asp															576
atc Ile	ggc Gly	gac Asp 195	ggc Gly	cct Pro	gtg Val	ctc Leu	ctc Leu 200	cca Pro	gac Asp	aac Asn	cat His	tac Tyr 205	ctg Leu	tcc Ser	acc Thr	624
cag Gln	tct Ser 210	gcc Ala	ctg Leu	tct Ser	aaa Lys	gat Asp 215	ccc Pro	aac Asn	gaa Glu	aag Lys	aga Arg 220	gac Asp	cac His	atg Met	gtc Val	672
ctg	cta	gag	+++	ata	acc	act	act	aaa	atc	202	cat	aac	ato	ac	ana	720

225 230 235 240

ctg tac aag tga
Leu Tyr Lys 732

<210> 50 <211> 243 <212> PRT

<213> Artificial Sequence

<400> 50

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Ser Val Ser Gly Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr 35 40 45

Leu Lys Phe Ile Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr 50 55 60

Leu Val Thr Thr Phe Ser Tyr Gly Val Gln Cys Phe Ser Arg Tyr Pro 65 70 75 80

Tyr Val Gln Glu Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys 100 105 110

Thr Arg Ala Glu Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile 115 120 125

Glu Leu Lys Gly Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His 130 135

Lys Leu Glu Tyr Asn Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp 145 150 155 160

Lys Gln Lys Asn Gly Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile \$165\$ \$170\$ \$175\$

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Glu Asp Gly Ser Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro
                                185
Ile Gly Asp Gly Pro Val Leu Leu Pro Asp Asn His Tyr Leu Ser Thr
                            200
Gln Ser Ala Leu Ser Lys Asp Pro Asn Glu Lys Arg Asp His Met Val
    210
                        215
Leu Leu Glu Phe Val Thr Ala Ala Gly Ile Thr His Gly Met Asp Glu
                    230
                                        235
Leu Tyr Lys
<210> 51
<211> 732
<212> DNA
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                  5
gtc cca att ctc gtg gaa ctg gat ggc gat gtg aat ggg cac aaa ttt
                                                                   96
Val Pro Ile Leu Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe
             20
tct gtc agc gga gag ggt gaa ggt gat gcc aca tac gga aag ctc acc
                                                                  144
Ser Val Ser Gly Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr
         35
                                                 45
ctg aaa ttc atc tgc acc act gga aag ctc cct gtg cca tgg cca aca
                                                                  192
Leu Lys Phe Ile Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr
     50
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ctg gtc act acc ttc tct tat ggc gtg cag tgc ttt tcc aga tac cca

۷ د 5	/al	Thr	Thr	Phe	Ser 70	Tyr	Gly	Val	Gln	Cys 75	Phe	Ser	Arg	Tyr	Pro 80	
														gag Glu 95		288
														tac Tyr		336
														aga Arg		384
ıl														ggc Gly		432
														gcc Ala		480
														aac Asn 175		528
														act Thr		576
														tcc Ser		624
n S														atg Met		672
g c u L 5	ctg Leu	gag Glu	ttt Phe	gtg Val	acc Thr 230	gct Ala	gct Ala	ggg Gly	atc Ile	aca Thr 235	cat His	ggc Gly	atg Met	gac Asp	gag Glu 240	720
_		aag Lvs	_													732

<210> 52

<211> 243

<212> PRT

<213> Artificial Sequence

<400> 52

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Val Pro Ile Leu Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe 20 25 30

Ser Val Ser Gly Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr 35 40 45

Leu Lys Phe Ile Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr 50 60

Leu Val Thr Thr Phe Ser Tyr Gly Val Gln Cys Phe Ser Arg Tyr Pro 65 70 75 80

Asp His Met Lys Gln His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly 85 90 95

Tyr Val Gln Glu Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys 100 105 110

Thr Arg Ala Glu Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile 115 120 125

Glu Leu Lys Gly Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His 130 135 140

Lys Leu Glu Tyr Asn Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp 145 150 155 160

Lys Gln Lys Asn Gly Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile 165 170 175

Glu Asp Gly Ser Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro
180 185

Ile Gly Asp Gly Pro Val Leu Leu Pro Asp Asn His Tyr Leu Ser Thr

195 200 205 Gln Ser Ala Leu Ser Lys Asp Pro Asn Glu Lys Arg Asp His Met Val 210 215 Leu Leu Glu Phe Val Thr Ala Ala Gly Ile Thr His Gly Met Asp Glu 230 235 Leu Tyr Lys <210> 53 <211> 732 <212> DNA <213> Artificial Sequence <220> <223> Description of Artificial Sequence: Ile(ATA)5GFP <220> <221> CDS <222> (1)..(732) <400> 53 atg ata ata ata ata agc aag ggc gag gaa ctg ttc act ggc gtg Met Ile Ile Ile Ile Ser Lys Gly Glu Glu Leu Phe Thr Gly Val gtc cca att ctc gtg gaa ctg gat ggc gat gtg aat ggg cac aaa ttt 96 Val Pro Ile Leu Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe 20 tct gtc agc gga gag ggt gaa ggt gat gcc aca tac gga aag ctc acc 144 Ser Val Ser Gly Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr 35 ctg aaa ttc atc tgc acc act gga aag ctc cct gtg cca tgg cca aca 192 Leu Lys Phe Ile Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr 50 5.5 ctg gtc act acc ttc tct tat ggc gtg cag tgc ttt tcc aga tac cca 240 Leu Val Thr Thr Phe Ser Tyr Gly Val Gln Cys Phe Ser Arg Tyr Pro 65 70 75 80 gac cat atg aag cag cat gac ttt ttc aag agc gcc atg ccc gag ggc 288

Asp	His	Met	Lys	Gln 85	His	Asp	Phe	Phe	Lys 90	Ser	Ala	Met	Pro	Glu 95	Gly	
tat Tyr	gtg Val	cag Gln	gag Glu 100	aga Arg	acc Thr	atc Ile	ttt Phe	ttc Phe 105	aaa Lys	gat Asp	gac Asp	ggg	aac Asn 110	tac Tyr	aag Lys	336
acc Thr	cgc Arg	gct Ala 115	gaa Glu	gtc Val	aag Lys	ttc Phe	gaa Glu 120	ggt Gly	gac Asp	acc Thr	ctg Leu	gtg Val 125	aat Asn	aga Arg	atc Ile	384
gag Glu	ctg Leu 130	aag Lys	ggc Gly	att Ile	gac Asp	ttt Phe 135	aag Lys	gag Glu	gat Asp	gga Gly	aac Asn 140	att Ile	ctc Leu	ggc Gly	cac His	432
aag Lys 145	ctg Leu	gaa Glu	tac Tyr	aac Asn	tat Tyr 150	aac Asn	tcc Ser	cac His	aat Asn	gtg Val 155	tac Tyr	atc Ile	atg Met	gcc Ala	gac Asp 160	480
aag Lys	caa Gln	aag Lys	aat Asn	ggc Gly 165	atc Ile	aag Lys	gtc Val	aac Asn	ttc Phe 170	aag Lys	atc Ile	aga Arg	cac His	aac Asn 175	att Ile	528
gag Glu	gat Asp	gga Gly	tcc Ser 180	gtg Val	cag Gln	ctg Leu	gcc Ala	gac Asp 185	cat His	tat Tyr	caa Gln	cag Gln	aac Asn 190	act Thr	cca Pro	576
atc Ile	ggc Gly	gac Asp 195	ggc Gly	cct Pro	gtg Val	ctc Leu	ctc Leu 200	cca Pro	gac Asp	aac Asn	cat His	tac Tyr 205	ctg Leu	tcc Ser	acc Thr	624
cag Gln	tct Ser 210	gcc Ala	ctg Leu	tct Ser	aaa Lys	gat Asp 215	ccc Pro	aac Asn	gaa Glu	aag Lys	aga Arg 220	gac Asp	cac His	atg Met	gtc Val	672
ctg Leu 225	ctg Leu	gag Glu	ttt Phe	gtg Val	acc Thr 230	gct Ala	gct Ala	Gly ggg	atc Ile	aca Thr 235	cat His	ggc Gly	atg Met	gac Asp	gag Glu 240	720
ctg Leu		aag Lys	tga													732

<210> 54 <211> 243 <212> PRT <213> Artificial Sequence

Val Pro Ile Leu Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe 20 25 30

Ser Val Ser Gly Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr 35 40 45

Leu Lys Phe Ile Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr 50 60

Leu Val Thr Thr Phe Ser Tyr Gly Val Gln Cys Phe Ser Arg Tyr Pro
65 70 75 80

Asp His Met Lys Gln His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly 85 90 95

Thr Arg Ala Glu Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile 115 120 125

Glu Leu Lys Gly Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His 130 135 140

Lys Leu Glu Tyr Asn Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp 145 150 155 160

Lys Gln Lys Asn Gly Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile 165 170 175

Glu Asp Gly Ser Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro $180 \,$

Ile Gly Asp Gly Pro Val Leu Leu Pro Asp Asn His Tyr Leu Ser Thr 195 200 205

Gln Ser Ala Leu Ser Lys Asp Pro Asn Glu Lys Arg Asp His Met Val 210 215 220

Leu 225	Leu	Glu	Phe	Val	Thr 230	Ala	Ala	Gly	Ile	Thr 235		Gly	Met	Asp	Glu 240	
Leu	Tyr	Lys														
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<220 <220	-	escr	ipti	on o	f Ar	tifi	cial	Seq	uenc	e: I	le(A	TC)5	GFP			
	l> C	DS 1)	(732)												
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gtc Val	cca Pro	att Ile	ctc Leu 20	gtg Val	gaa Glu	ctg Leu	gat Asp	ggc Gly 25	gat Asp	gtg Val	aat Asn	ggg Gly	cac His 30	aaa Lys	ttt Phe	96
tct Ser	gtc Val	agc Ser 35	gga Gly	gag Glu	ggt Gly	gaa Glu	ggt Gly 40	gat Asp	gcc Ala	aca Thr	tac Tyr	gga Gly 45	aag Lys	ctc Leu	acc Thr	144
ctg Leu	aaa Lys 50	ttc Phe	atc Ile	tgc Cys	acc Thr	act Thr 55	gga Gly	aag Lys	ctc Leu	cct Pro	gtg Val 60	cca Pro	tgg Trp	cca Pro	aca Thr	192
ctg Leu 65	gtc Val	act Thr	acc Thr	ttc Phe	tct Ser 70	tat Tyr	ggc Gly	gtg Val	cag Gln	tgc Cys 75	ttt Phe	tcc Ser	aga Arg	tac Tyr	cca Pro 80	240
gac Asp	cat His	atg Met	aag Lys	cag Gln 85	cat His	gac Asp	ttt Phe	ttc Phe	aag Lys 90	agc Ser	gcc Ala	atg Met	ccc Pro	gag Glu 95	ggc Gly	288
tat	gtg	cag	gag	aga	acc	atc	ttt	ttc	aaa	gat	gac	ggg	aac	tac	aag	336

Tyr	Val	Gln	Glu 100	Arg	Thr	Ile	Phe	Phe 105	Lys	Asp	Asp	Gly	Asn 110	Tyr	Lys	
acc Thr	cgc Arg	gct Ala 115	gaa Glu	gtc Val	aag Lys	ttc Phe	gaa Glu 120	ggt Gly	gac Asp	acc Thr	ctg Leu	gtg Val 125	aat Asn	aga Arg	atc Ile	384
gag Glu	ctg Leu 130	aag Lys	ggc Gly	att Ile	gac Asp	ttt Phe 135	aag Lys	gag Glu	gat Asp	gga Gly	aac Asn 140	att Ile	ctc Leu	ggc Gly	cac His	432
aag Lys 145	ctg Leu	gaa Glu	tac Tyr	aac Asn	tat Tyr 150	aac Asn	tcc Ser	cac His	aat Asn	gtg Val 155	tac Tyr	atc Ile	atg Met	gcc Ala	gac Asp 160	480
aag Lys	caa Gln	aag Lys	aat Asn	ggc Gly 165	atc Ile	aag Lys	gtc Val	aac Asn	ttc Phe 170	aag Lys	atc Ile	aga Arg	cac His	aac Asn 175	att Ile	528
gag Glu	gat Asp	gga Gly	tcc Ser 180	gtg Val	cag Gln	ctg Leu	gcc Ala	gac Asp 185	cat His	tat Tyr	caa Gln	cag Gln	aac Asn 190	act Thr	cca Pro	576
atc Ile	ggc Gly	gac Asp 195	ggc Gly	cct Pro	gtg Val	ctc Leu	ctc Leu 200	cca Pro	gac Asp	aac Asn	cat His	tac Tyr 205	ctg Leu	tcc Ser	acc Thr	624
cag Gln	tct Ser 210	gcc Ala	ctg Leu	tct Ser	aaa Lys	gat Asp 215	ccc Pro	aac Asn	gaa Glu	aag Lys	aga Arg 220	gac Asp	cac His	atg Met	gtc Val	672
ctg Leu 225	ctg Leu	gag Glu	ttt Phe	gtg Val	acc Thr 230	gct Ala	gct Ala	ggg Gly	atc Ile	aca Thr 235	cat His	ggc Gly	atg Met	gac Asp	gag Glu 240	720
	tac Tyr	aag Lys	tga													732

<210> 56 <211> 243 <212> PRT <213> Artificial Sequence

<400> 56

Met Ile Ile Ile Ile Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr Phe Ser Tyr Gly Val Gln Cys Phe Ser Arg Tyr Pro Asp His Met Lys Gln His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile 115 Glu Leu Lys Gly Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His 135 Lys Leu Glu Tyr Asn Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp 150 Lys Gln Lys Asn Gly Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile Glu Asp Gly Ser Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro 185 Ile Gly Asp Gly Pro Val Leu Leu Pro Asp Asn His Tyr Leu Ser Thr 200 Gln Ser Ala Leu Ser Lys Asp Pro Asn Glu Lys Arg Asp His Met Val

215

230

Leu Leu Glu Phe Val Thr Ala Ala Gly Ile Thr His Gly Met Asp Glu

Leu Tyr Lys

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<210> 57
<211> 732
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gtc cca att ctc gtg gaa ctg gat ggc gat gtg aat ggg cac aaa ttt
                                                                   96
Val Pro Ile Leu Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe
tct gtc agc gga gag ggt gaa ggt gat gcc aca tac gga aag ctc acc
Ser Val Ser Gly Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr
ctg aaa ttc atc tgc acc act gga aag ctc cct gtg cca tgg cca aca
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Leu Lys Phe Ile Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr
     50
ctg gtc act acc ttc tct tat ggc gtg cag tgc ttt tcc aga tac cca
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Leu Val Thr Thr Phe Ser Tyr Gly Val Gln Cys Phe Ser Arg Tyr Pro
65
                     70
gac cat atg aag cag cat gac ttt ttc aag agc gcc atg ccc gag ggc
                                                                   288
Asp His Met Lys Gln His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly
                 85
tat gtg cag gag aga acc atc ttt ttc aaa gat gac ggg aac tac aag
                                                                  336
Tyr Val Gln Glu Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys
            100
                                105
acc cgc gct gaa gtc aag ttc gaa ggt gac acc ctg gtg aat aga atc
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Thr	Arg	Ala 115	Glu	Val	Lys	Phe	Glu 120	Gly	Asp	Thr	Leu	Val 125	Asn	Arg	Ile	
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aag Lys 145	ctg Leu	gaa Glu	tac Tyr	aac Asn	tat Tyr 150	aac Asn	tcc Ser	cac His	aat Asn	gtg Val 155	tac Tyr	atc Ile	atg Met	gcc Ala	gac Asp 160	480
aag Lys	caa Gln	aag Lys	aat Asn	ggc Gly 165	atc Ile	aag Lys	gtc Val	aac Asn	ttc Phe 170	aag Lys	atc Ile	aga Arg	cac His	aac Asn 175	att Ile	528
gag Glu	gat Asp	gga Gly	tcc Ser 180	gtg Val	cag Gln	ctg Leu	gcc Ala	gac Asp 185	cat His	tat Tyr	caa Gln	cag Gln	aac Asn 190	act Thr	cca Pro	576
atc Ile	ggc Gly	gac Asp 195	ggc Gly	cct Pro	gtg Val	ctc Leu	ctc Leu 200	cca Pro	gac Asp	aac Asn	cat His	tac Tyr 205	ctg Leu	tcc Ser	acc Thr	624
cag Gln	tct Ser 210	gcc Ala	ctg Leu	tct Ser	aaa Lys	gat Asp 215	ccc Pro	aac Asn	gaa Glu	aag Lys	aga Arg 220	gac Asp	cac His	atg Met	gtc Val	672
ctg Leu 225	ctg Leu	gag Glu	ttt Phe	gtg Val	acc Thr 230	gct Ala	gct Ala	ggg Gly	atc Ile	aca Thr 235	cat His	ggc Gly	atg Met	gac Asp	gag Glu 240	720
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Val	Pro	Ile	Leu	Val	Glu	Leu	Asp	Gly	Asp	Val	Asn	Gly	His	Lys	Phe	

20 25 30

Ser Val Ser Gly Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr

Leu Lys Phe Ile Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr

Leu Val Thr Thr Phe Ser Tyr Gly Val Gln Cys Phe Ser Arg Tyr Pro

Asp His Met Lys Gln His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly

Tyr Val Gln Glu Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys 105

Thr Arg Ala Glu Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile 115

Glu Leu Lys Gly Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His 135

Lys Leu Glu Tyr Asn Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp 145 150

Lys Gln Lys Asn Gly Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile 165 170

Glu Asp Gly Ser Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro 180

Ile Gly Asp Gly Pro Val Leu Leu Pro Asp Asn His Tyr Leu Ser Thr 200

Gln Ser Ala Leu Ser Lys Asp Pro Asn Glu Lys Arg Asp His Met Val

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Leu Tyr Lys

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Val Pro Ile Leu Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe
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tct gtc agc gga gag ggt gaa ggt gat gcc aca tac gga aag ctc acc
Ser Val Ser Gly Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr
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Leu Lys Phe Ile Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr
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ctg gtc act acc ttc tct tat ggc gtg cag tgc ttt tcc aga tac cca
                                                                   240
Leu Val Thr Thr Phe Ser Tyr Gly Val Gln Cys Phe Ser Arg Tyr Pro
65
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gac cat atg aag cag cat gac ttt ttc aag agc gcc atg ccc gag ggc
                                                                   288
Asp His Met Lys Gln His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly
                 85
tat gtg cag gag aga acc atc ttt ttc aaa gat gac ggg aac tac aag
                                                                   336
Tyr Val Gln Glu Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys
            100
                                105
acc cgc gct gaa gtc aag ttc gaa ggt gac acc ctg gtg aat aga atc
                                                                  384
Thr Arg Ala Glu Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile
        115
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gag Glu	gat Asp	gga Gly	tcc Ser 180	gtg Val	cag Gln	ctg Leu	gcc Ala	gac Asp 185	cat His	tat Tyr	caa Gln	cag Gln	aac Asn 190	act Thr	cca Pro	576
atc Ile	ggc Gly	gac Asp 195	ggc Gly	cct Pro	gtg Val	ctc Leu	ctc Leu 200	cca Pro	gac Asp	aac Asn	cat His	tac Tyr 205	ctg Leu	tcc Ser	acc Thr	624
cag Gln	tct Ser 210	gcc Ala	ctg Leu	tct Ser	aaa Lys	gat Asp 215	ccc Pro	aac Asn	gaa Glu	aag Lys	aga Arg 220	gac Asp	cac His	atg Met	gtc Val	672
ctg Leu 225	ctg Leu	gag Glu	ttt Phe	gtg Val	acc Thr 230	gct Ala	gct Ala	ggg Gly	atc Ile	aca Thr 235	cat His	ggc Gly	atg Met	gac Asp	gag Glu 240	720
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Ser	Val	Ser 35	Gly	Glu	Gly	Glu	Gly 40	Asp	Ala	Thr	Tyr	Gly 45	Lys	Leu	Thr	

Leu Lys Phe Ile Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr 50 60

Leu Val Thr Thr Phe Ser Tyr Gly Val Gln Cys Phe Ser Arg Tyr Pro 65 70 75 80

Asp His Met Lys Gln His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly 85 90 95

Thr Arg Ala Glu Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile 115 120 125

Glu Leu Lys Gly Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His 130 135 140

Lys Leu Glu Tyr Asn Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp 145 150 155 160

Lys Gln Lys Asn Gly Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile 165 170 175

Ile Gly Asp Gly Pro Val Leu Leu Pro Asp Asn His Tyr Leu Ser Thr 195 200 205

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Leu Tyr Lys

<210> 61

<211> 732

<212> DNA

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					gaa Glu											96
					ggt Gly											144
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					tct Ser 70											240
					cat His											288
					acc Thr											336
					aag Lys											384
					gac Asp											432
aag	ctg	gaa	tac	aac	tat	aac	tcc	cac	aat	gtg	tac	atc	atg	gcc	gac	480

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gag Glu	gat Asp	gga Gly	tcc Ser 180	gtg Val	cag Gln	ctg Leu	gcc Ala	gac Asp 185	cat His	tat Tyr	caa Gln	cag Gln	aac Asn 190	act Thr	cca Pro	576
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cag Gln	tct Ser 210	gcc Ala	ctg Leu	tct Ser	aaa Lys	gat Asp 215	ccc Pro	aac Asn	gaa Glu	aag Lys	aga Arg 220	gac Asp	cac His	atg Met	gtc Val	672
ctg Leu 225	ctg Leu	gag Glu	ttt Phe	gtg Val	acc Thr 230	gct Ala	gct Ala	Gly ggg	atc Ile	aca Thr 235	cat His	ggc Gly	atg Met	gac Asp	gag Glu 240	720
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Ser	Val	Ser 35	Gly	Glu	Gly	Glu	Gly 40	Asp	Ala	Thr	Tyr	Gly 45	Lys	Leu	Thr	
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Ile Gly Asp Gly Pro Val Leu Leu Pro Asp Asn His Tyr Leu Ser Thr 195 200 205

Gln Ser Ala Leu Ser Lys Asp Pro Asn Glu Lys Arg Asp His Met Val 210 215 220

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Leu Tyr Lys

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<211> 732

<212> DNA

<213> Artificial Sequence

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<223> Description of Artificial Sequence: Leu(CTG)5GFP

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aag ctg gaa tac aac tat aac tcc cac aat gtg tac atc atg gcc gac

Lys Leu Glu Tyr Asn Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp

aag caa aag aat ggc atc aag gtc aac ttc aag atc aga cac aac att

150

155

480

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atc Ile	ggc Gly	gac Asp 195	ggc Gly	cct Pro	gtg Val	ctc Leu	ctc Leu 200	cca Pro	gac Asp	aac Asn	cat His	tac Tyr 205	ctg Leu	tcc Ser	acc Thr	624
cag Gln	tct Ser 210	gcc Ala	ctg Leu	tct Ser	aaa Lys	gat Asp 215	ccc Pro	aac Asn	gaa Glu	aag Lys	aga Arg 220	gac Asp	cac His	atg Met	gtc Val	672
ctg Leu 225	ctg Leu	gag Glu	ttt Phe	gtg Val	acc Thr 230	gct Ala	gct Ala	ggg Gly	atc Ile	aca Thr 235	cat His	ggc Gly	atg Met	gac Asp	gag Glu 240	720
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Ser	Val	Ser 35	Gly	Glu	Gly	Glu	Gly 40	Asp	Ala	Thr	Tyr	Gly 45	Lys	Leu	Thr	
Leu	Lys 50	Phe	Ile	Cys	Thr	Thr 55	Gly	Lys	Leu	Pro	Val 60	Pro	Trp	Pro	Thr	
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Lys Leu Glu Tyr Asn Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp
Lys Gln Lys Asn Gly Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile
Glu Asp Gly Ser Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro
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Ile Gly Asp Gly Pro Val Leu Leu Pro Asp Asn His Tyr Leu Ser Thr
Gln Ser Ala Leu Ser Lys Asp Pro Asn Glu Lys Arg Asp His Met Val
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gtc Val	cca Pro	att Ile	ctc Leu 20	gtg Val	gaa Glu	ctg Leu	gat Asp	ggc Gly 25	gat Asp	gtg Val	aat Asn	ggg Gly	cac His 30	aaa Lys	ttt Phe	96
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ctg Leu	aaa Lys 50	ttc Phe	atc Ile	tgc Cys	acc Thr	act Thr 55	gga Gly	aag Lys	ctc Leu	cct Pro	gtg Val 60	cca Pro	tgg Trp	cca Pro	aca Thr	192
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tat Tyr	gtg Val	cag Gln	gag Glu 100	aga Arg	acc Thr	atc Ile	ttt Phe	ttc Phe 105	aaa Lys	gat Asp	gac Asp	Gly	aac Asn 110	tac Tyr	aag Lys	336
acc Thr	cgc Arg	gct Ala 115	gaa Glu	gtc Val	aag Lys	ttc Phe	gaa Glu 120	ggt Gly	gac Asp	acc Thr	ctg Leu	gtg Val 125	aat Asn	aga Arg	atc Ile	384
gag Glu	ctg Leu 130	aag Lys	ggc Gly	att Ile	gac Asp	ttt Phe 135	aag Lys	gag Glu	gat Asp	gga Gly	aac Asn 140	att Ile	ctc Leu	ggc Gly	cac His	432
aag Lys 145	ctg Leu	gaa Glu	tac Tyr	aac Asn	tat Tyr 150	aac Asn	tcc Ser	cac His	aat Asn	gtg Val 155	tac Tyr	atc Ile	atg Met	gcc Ala	gac Asp 160	480
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	ggc Gly															624
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ctg Leu 225	ctg Leu	gag Glu	ttt Phe	gtg Val	acc Thr 230	gct Ala	gct Ala	ggg Gly	atc Ile	aca Thr 235	cat His	ggc Gly	atg Met	gac Asp	gag Glu 240	720
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Leu 65	Val	Thr	Thr	Phe	Ser 70	Tyr	Gly	Val	Gln	Cys 75	Phe	Ser	Arg	Tyr	Pro 80	

Tyr Val Gln Glu Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys 100 105 110

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Lys Gln Lys Asn Gly Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile
Glu Asp Gly Ser Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro
Ile Gly Asp Gly Pro Val Leu Leu Pro Asp Asn His Tyr Leu Ser Thr
Gln Ser Ala Leu Ser Lys Asp Pro Asn Glu Lys Arg Asp His Met Val
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Leu Tyr Lys
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ctg Leu	aaa Lys 50	ttc Phe	atc Ile	tgc Cys	acc Thr	act Thr 55	gga Gly	aag Lys	ctc Leu	cct Pro	gtg Val 60	cca Pro	tgg Trp	cca Pro	aca Thr	192
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aag Lys 145	ctg Leu	gaa Glu	tac Tyr	aac Asn	tat Tyr 150	aac Asn	tcc Ser	cac His	aat Asn	gtg Val 155	tac Tyr	atc Ile	atg Met	gcc Ala	gac Asp 160	480
aag Lys	caa Gln	aag Lys	aat Asn	ggc Gly 165	atc Ile	aag Lys	gtc Val	aac Asn	ttc Phe 170	aag Lys	atc Ile	aga Arg	cac His	aac Asn 175	att Ile	528
gag Glu	gat Asp	gga Gly	tcc Ser 180	gtg Val	cag Gln	ctg Leu	gcc Ala	gac Asp 185	cat His	tat Tyr	caa Gln	cag Gln	aac Asn 190	act Thr	cca Pro	576
atc	ggc	gac	ggc	cct	gtg	ctc	ctc	cca	gac	aac	cat	tac	ctg	tcc	acc	624

Ile	Gly	Asp 195	Gly	Pro	Val	Leu	Leu 200	Pro	Asp	Asn	His	Tyr 205	Leu	Ser	Thr	
cag Gln	tct Ser 210	gcc Ala	ctg Leu	tct Ser	aaa Lys	gat Asp 215	ccc Pro	aac Asn	gaa Glu	aag Lys	aga Arg 220	gac Asp	cac His	atg Met	gtc Val	672
ctg Leu 225	ctg Leu	gag Glu	ttt Phe	gtg Val	acc Thr 230	gct Ala	gct Ala	ggg	atc Ile	aca Thr 235	cat His	ggc Gly	atg Met	gac Asp	gag Glu 240	720
	tac Tyr	aag Lys	tga													732
<210> 68 <211> 243 <212> PRT <213> Artificial Sequence																
)> 68 Leu	B Leu	Leu	Leu 5	Leu	Ser	Lys	Gly	Glu 10	Glu	Leu	Phe	Thr	Gly 15	Val	
Val	Pro	Ile	Leu 20	Val	Glu	Leu	Asp	Gly 25	Asp	Val	Asn	Gly	His 30	Lys	Phe	
Ser	Val	Ser 35	Gly	Glu	Gly	Glu	Gly 40	Asp	Ala	Thr	Tyr	Gly 45	Lys	Leu	Thr	
Leu	Lys 50	Phe	Ile	Cys	Thr	Thr 55	Gly	Lys	Leu	Pro	Val 60	Pro	Trp	Pro	Thr	
Leu 65	Val	Thr	Thr	Phe	Ser 70	Tyr	Gly	Val	Gln	Cys 75	Phe	Ser	Arg	Tyr	Pro 80	
Asp	His	Met	Lys	Gln 85	His	Asp	Phe	Phe	Lys 90	Ser	Ala	Met	Pro	Glu 95	Gly	

Tyr Val Gln Glu Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys

Thr Arg Ala Glu Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile

120

105

100

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Glu Leu Lys Gly Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His
                        135
Lys Leu Glu Tyr Asn Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp
                    150
Lys Gln Lys Asn Gly Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile
Glu Asp Gly Ser Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro
Ile Gly Asp Gly Pro Val Leu Leu Pro Asp Asn His Tyr Leu Ser Thr
Gln Ser Ala Leu Ser Lys Asp Pro Asn Glu Lys Arg Asp His Met Val
    210
                        215
Leu Leu Glu Phe Val Thr Ala Ala Gly Ile Thr His Gly Met Asp Glu
225
                    230
Leu Tyr Lys
<210> 69
<211> 732
<212> DNA
<213> Artificial Sequence
<223> Description of Artificial Sequence: Leu(TTG)5GFP
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<222> (1)..(732)
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Met Leu Leu Leu Leu Ser Lys Gly Glu Glu Leu Phe Thr Gly Val
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gtc cca att ctc gtg gaa ctg gat ggc gat gtg aat ggg cac aaa ttt
                                                                   96
Val Pro Ile Leu Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe
             20
                                 25
                                                     30
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tct Ser	gtc Val	agc Ser 35	gga Gly	gag Glu	ggt Gly	gaa Glu	ggt Gly 40	gat Asp	gcc Ala	aca Thr	tac Tyr	gga Gly 45	aag Lys	ctc Leu	acc Thr	144
ctg Leu	aaa Lys 50	ttc Phe	atc Ile	tgc Cys	acc Thr	act Thr 55	gga Gly	aag Lys	ctc Leu	cct Pro	gtg Val 60	cca Pro	tgg Trp	cca Pro	aca Thr	192
ctg Leu 65	gtc Val	act Thr	acc Thr	ttc Phe	tct Ser 70	tat Tyr	ggc Gly	gtg Val	cag Gln	tgc Cys 75	ttt Phe	tcc Ser	aga Arg	tac Tyr	cca Pro 80	240
gac Asp	cat His	atg Met	aag Lys	cag Gln 85	cat His	gac Asp	ttt Phe	ttc Phe	aag Lys 90	agc Ser	gcc Ala	atg Met	ccc Pro	gag Glu 95	ggc Gly	288
tat Tyr	gtg Val	cag Gln	gag Glu 100	aga Arg	acc Thr	atc Ile	ttt Phe	ttc Phe 105	aaa Lys	gat Asp	gac Asp	Gly ggg	aac Asn 110	tac Tyr	aag Lys	336
acc Thr	cgc Arg	gct Ala 115	gaa Glu	gtc Val	aag Lys	ttc Phe	gaa Glu 120	ggt Gly	gac Asp	acc Thr	ctg Leu	gtg Val 125	aat Asn	aga Arg	atc Ile	384
gag Glu	ctg Leu 130	aag Lys	ggc Gly	att Ile	gac Asp	ttt Phe 135	aag Lys	gag Glu	gat Asp	gga Gly	aac Asn 140	att Ile	ctc Leu	ggc Gly	cac His	432
aag Lys 145	ctg Leu	gaa Glu	tac Tyr	aac Asn	tat Tyr 150	aac Asn	tcc Ser	cac His	aat Asn	gtg Val 155	tac Tyr	atc Ile	atg Met	gcc Ala	gac Asp 160	480
aag Lys	caa Gln	aag Lys	aat Asn	ggc Gly 165	atc Ile	aag Lys	gtc Val	aac Asn	ttc Phe 170	aag Lys	atc Ile	aga Arg	cac His	aac Asn 175	att Ile	528
gag Glu	gat Asp	gga Gly	tcc Ser 180	gtg Val	cag Gln	ctg Leu	gcc Ala	gac Asp 185	cat His	tat Tyr	caa Gln	cag Gln	aac Asn 190	act Thr	cca Pro	576
atc Ile	ggc Gly	gac Asp 195	ggc Gly	cct Pro	gtg Val	ctc Leu	ctc Leu 200	cca Pro	gac Asp	aac Asn	cat His	tac Tyr 205	ctg Leu	tcc Ser	acc Thr	624
cag	tct	gcc	ctg	tct	aaa	gat	CCC	aac	gaa	aag	aga	gac	cac	atg	gtc	672

Gln	Ser 210	Ala	Leu	Ser	Lys	Asp 215	Pro	Asn	Glu	Lys	Arg 220	Asp	His	Met	Val	
ctg Leu 225	ctg Leu	gag Glu	ttt Phe	gtg Val	acc Thr 230	gct Ala	gct Ala	gly ggg	atc Ile	aca Thr 235	cat His	ggc Gly	atg Met	gac Asp	gag Glu 240	720
	tac Tyr	aag Lys	tga													732
<210> 70 <211> 243 <212> PRT <213> Artificial Sequence <400> 70																
			Leu	Leu 5	Leu	Ser	Lys	Gly	Glu 10	Glu	Leu	Phe	Thr	Gly 15	Val	
Val	Pro	Ile	Leu 20	Val	Glu	Leu	Asp	Gly 25	Asp	Val	Asn	Gly	His 30	Lys	Phe	
Ser	Val	Ser 35	Gly	Glu	Gly	Glu	Gly 40	Asp	Ala	Thr	Tyr	Gly 45	Lys	Leu	Thr	
Leu	Lys 50	Phe	Ile	Cys	Thr	Thr 55	Gly	Lys	Leu	Pro	Val 60	Pro	Trp	Pro	Thr	
Leu 65	Val	Thr	Thr	Phe	Ser 70	Tyr	Gly	Val	Gln	Cys 75	Phe	Ser	Arg	Tyr	Pro 80	
Asp	His	Met	Lys	Gln 85	His	Asp	Phe	Phe	Lys 90	Ser	Ala	Met	Pro	Glu 95	Gly	
Tyr	Val	Gln	Glu 100	Arg	Thr	Ile	Phe	Phe 105	Lys	Asp	Asp	Gly	Asn 110	Tyr	Lys	
Thr	Arg	Ala 115	Glu	Val	Lys	Phe	Glu 120	Gly	Asp	Thr	Leu	Val 125	Asn	Arg	Ile	
Glu	Leu 130	Lys	Gly	Ile	Asp	Phe 135	Lys	Glu	Asp	Gly	Asn 140	Ile	Leu	Gly	His	
Lys	Leu	Glu	Tyr	Asn	Tyr	Asn	Ser	His	Asn	Val	Tyr	Ile	Met	Ala	Asp	

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145
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                                        155
                                                            160
Lys Gln Lys Asn Gly Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile
                                    170
Glu Asp Gly Ser Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro
Ile Gly Asp Gly Pro Val Leu Leu Pro Asp Asn His Tyr Leu Ser Thr
Gln Ser Ala Leu Ser Lys Asp Pro Asn Glu Lys Arg Asp His Met Val
    210
                        215
Leu Leu Glu Phe Val Thr Ala Ala Gly Ile Thr His Gly Met Asp Glu
225
                    230
                                        235
Leu Tyr Lys
<210> 71
<211> 732
<212> DNA
<213> Artificial Sequence
<220>
<223> Description of Artificial Sequence: Lys(AAA)5GFP
<220>
<221> CDS
<222> (1)..(732)
<400> 71
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Met Lys Lys Lys Lys Ser Lys Gly Glu Glu Leu Phe Thr Gly Val
                                     10
gtc cca att ctc gtg gaa ctg gat ggc gat gtg aat ggg cac aaa ttt
                                                                   96
Val Pro Ile Leu Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe
                                 25
tet gte age gga gag ggt gaa ggt gat gee aca tae gga aag ete ace
                                                                   144
Ser Val Ser Gly Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr
                             40
                                                 45
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ctg Leu	aaa Lys 50	ttc Phe	atc Ile	tgc Cys	acc Thr	act Thr 55	gga Gly	aag Lys	ctc Leu	cct Pro	gtg Val 60	cca Pro	tgg Trp	cca Pro	aca Thr	192
ctg Leu 65	gtc Val	act Thr	acc Thr	ttc Phe	tct Ser 70	tat Tyr	ggc Gly	gtg Val	cag Gln	tgc Cys 75	ttt Phe	tcc Ser	aga Arg	tac Tyr	cca Pro 80	240
gac Asp	cat His	atg Met	aag Lys	cag Gln 85	cat His	gac Asp	ttt Phe	ttc Phe	aag Lys 90	agc Ser	gcc Ala	atg Met	ccc Pro	gag Glu 95	ggc Gly	288
tat Tyr	gtg Val	cag Gln	gag Glu 100	aga Arg	acc Thr	atc Ile	ttt Phe	ttc Phe 105	aaa Lys	gat Asp	gac Asp	ggg Gly	aac Asn 110	tac Tyr	aag Lys	336
acc Thr	cgc Arg	gct Ala 115	gaa Glu	gtc Val	aag Lys	ttc Phe	gaa Glu 120	ggt Gly	gac Asp	acc Thr	ctg Leu	gtg Val 125	aat Asn	aga Arg	atc Ile	384
gag Glu	ctg Leu 130	aag Lys	ggc Gly	att Ile	gac Asp	ttt Phe 135	aag Lys	gag Glu	gat Asp	gga Gly	aac Asn 140	att Ile	ctc Leu	ggc Gly	cac His	432
aag Lys 145	ctg Leu	gaa Glu	tac Tyr	aac Asn	tat Tyr 150	aac Asn	tcc Ser	cac His	aat Asn	gtg Val 155	tac Tyr	atc Ile	atg Met	gcc Ala	gac Asp 160	480
aag Lys	caa Gln	aag Lys	aat Asn	ggc Gly 165	atc Ile	aag Lys	gtc Val	aac Asn	ttc Phe 170	aag Lys	atc Ile	aga Arg	cac His	aac Asn 175	att Ile	528
gag Glu	gat Asp	gga Gly	tcc Ser 180	gtg Val	cag Gln	ctg Leu	gcc Ala	gac Asp 185	cat His	tat Tyr	caa Gln	cag Gln	aac Asn 190	act Thr	cca Pro	576
atc Ile	ggc Gly	gac Asp 195	ggc Gly	cct Pro	gtg Val	ctc Leu	ctc Leu 200	cca Pro	gac Asp	aac Asn	cat His	tac Tyr 205	ctg Leu	tcc Ser	acc Thr	624
cag Gln	tct Ser 210	gcc Ala	ctg Leu	tct Ser	aaa Lys	gat Asp 215	ccc Pro	aac Asn	gaa Glu	aag Lys	aga Arg 220	gac Asp	cac His	atg Met	gtc Val	672
ctg	ctg	gag	ttt	gtg	acc	gct	gct	ggg	atc	aca	cat	ggc	atg	gac	gag	720

Leu Leu Glu Phe Val Thr Ala Ala Gly Ile Thr His Gly Met Asp Glu 230 732 ctg tac aag tga Leu Tyr Lys <210> 72 <211> 243 <212> PRT <213> Artificial Sequence <400> 72 Met Lys Lys Lys Lys Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr Phe Ser Tyr Gly Val Gln Cys Phe Ser Arg Tyr Pro 70 Asp His Met Lys Gln His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys 105 110 Thr Arg Ala Glu Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr Asn Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp Lys Gln Lys Asn Gly Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile 170

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Glu Asp Gly Ser Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro
Ile Gly Asp Gly Pro Val Leu Leu Pro Asp Asn His Tyr Leu Ser Thr
Gln Ser Ala Leu Ser Lys Asp Pro Asn Glu Lys Arg Asp His Met Val
Leu Leu Glu Phe Val Thr Ala Ala Gly Ile Thr His Gly Met Asp Glu
                                        235
Leu Tyr Lys
<210> 73
<211> 732
<212> DNA
<213> Artificial Sequence
<223> Description of Artificial Sequence: Lys(AAG)5GFP
<220>
<221> CDS
<222> (1)..(732)
<400> 73
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Met Lys Lys Lys Lys Ser Lys Gly Glu Glu Leu Phe Thr Gly Val
                                     10
gtc cca att ctc gtg gaa ctg gat ggc gat gtg aat ggg cac aaa ttt
                                                                   96
Val Pro Ile Leu Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe
             20
tot gto ago gga gag ggt gaa ggt gat gco aca tac gga aag cto acc
                                                                   144
Ser Val Ser Gly Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr
ctg aaa ttc atc tgc acc act gga aag ctc cct gtg cca tgg cca aca
                                                                   192
Leu Lys Phe Ile Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr
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55

									tac Tyr		240
									gag Glu 95		288
									tac Tyr		336
									aga Arg		384
									ggc Gly		432
_	_	_						_	gcc Ala	_	480
									aac Asn 175		528
									act Thr		576
									tcc Ser		624
									atg Met		672
									gac Asp		720
ctg	tac	aag	tga								732

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Leu Tyr Lys
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<210> 74

<211> 243

<212> PRT

<213> Artificial Sequence

<400> 74

Met Lys Lys Lys Lys Ser Lys Gly Glu Glu Leu Phe Thr Gly Val
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Val Pro Ile Leu Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe 20 25 30

Ser Val Ser Gly Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr 35 40 45

Leu Lys Phe Ile Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr 50 60

Leu Val Thr Thr Phe Ser Tyr Gly Val Gln Cys Phe Ser Arg Tyr Pro
65 70 75 80

Asp His Met Lys Gln His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly
85 90 95

Thr Arg Ala Glu Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile 115 120 125

Glu Leu Lys Gly Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His 130 135 140

Lys Leu Glu Tyr Asn Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp 145 150 155 160

Lys Gln Lys Asn Gly Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile 165 170 175

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Ile Gly Asp Gly Pro Val Leu Leu Pro Asp Asn His Tyr Leu Ser Thr
Gln Ser Ala Leu Ser Lys Asp Pro Asn Glu Lys Arg Asp His Met Val
Leu Leu Glu Phe Val Thr Ala Ala Gly Ile Thr His Gly Met Asp Glu
Leu Tyr Lys
<210> 75
<211> 732
<212> DNA
<213> Artificial Sequence
<220>
<223> Description of Artificial Sequence: Phe(TTT)5GFP
<220>
<221> CDS
<222> (1)..(732)
<400> 75
atg ttt ttt ttt ttt agc aag ggc gag gaa ctg ttc act ggc gtg
                                                                   48
Met Phe Phe Phe Phe Ser Lys Gly Glu Glu Leu Phe Thr Gly Val
gtc cca att ctc gtg gaa ctg gat ggc gat gtg aat ggg cac aaa ttt
                                                                   96
Val Pro Ile Leu Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe
             20
                                 25
tct gtc agc gga gag ggt gaa ggt gat gcc aca tac gga aag ctc acc
                                                                  144
Ser Val Ser Gly Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr
                             40
ctg aaa ttc atc tgc acc act gga aag ctc cct gtg cca tgg cca aca
                                                                  192
Leu Lys Phe Ile Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr
                         55
ctg gtc act acc ttc tct tat ggc gtg cag tgc ttt tcc aga tac cca
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Leu Val Thr Thr Phe Ser Tyr Gly Val Gln Cys Phe Ser Arg Tyr Pro

70

75

				cag Gln 85												288
				aga Arg												336
acc Thr	cgc Arg	gct Ala 115	gaa Glu	gtc Val	aag Lys	ttc Phe	gaa Glu 120	ggt Gly	gac Asp	acc Thr	ctg Leu	gtg Val 125	aat Asn	aga Arg	atc Ile	384
gag Glu	ctg Leu 130	aag Lys	ggc Gly	att Ile	gac Asp	ttt Phe 135	aag Lys	gag Glu	gat Asp	gga Gly	aac Asn 140	att Ile	ctc Leu	ggc Gly	cac His	432
				aac Asn												480
aag Lys	caa Gln	aag Lys	aat Asn	ggc Gly 165	atc Ile	aag Lys	gtc Val	aac Asn	ttc Phe 170	aag Lys	atc Ile	aga Arg	cac His	aac Asn 175	att Ile	528
gag Glu	gat Asp	gga Gly	tcc Ser 180	gtg Val	cag Gln	ctg Leu	gcc Ala	gac Asp 185	cat His	tat Tyr	caa Gln	cag Gln	aac Asn 190	act Thr	cca Pro	576
atc Ile	ggc Gly	gac Asp 195	ggc Gly	cct Pro	gtg Val	ctc Leu	ctc Leu 200	cca Pro	gac Asp	aac Asn	cat His	tac Tyr 205	ctg Leu	tcc Ser	acc Thr	624
cag Gln	tct Ser 210	gcc Ala	ctg Leu	tct Ser	aaa Lys	gat Asp 215	ccc Pro	aac Asn	gaa Glu	aag Lys	aga Arg 220	gac Asp	cac His	atg Met	gtc Val	672
ctg Leu 225	ctg Leu	gag Glu	ttt Phe	gtg Val	acc Thr 230	gct Ala	gct Ala	ggg Gly	atc Ile	aca Thr 235	cat His	ggc Gly	atg Met	gac Asp	gag Glu 240	720
	tac Tyr	aag Lys	tga													732

<210> 76

- <211> 243
- <212> PRT
- <213> Artificial Sequence
- <400> 76
- Met Phe Phe Phe Phe Ser Lys Gly Glu Glu Leu Phe Thr Gly Val
- Val Pro Ile Leu Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe 20 25 30
- Ser Val Ser Gly Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr 35 40 45
- Leu Lys Phe Ile Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr 50 55 60
- Leu Val Thr Thr Phe Ser Tyr Gly Val Gln Cys Phe Ser Arg Tyr Pro 65 70 75 80
- Asp His Met Lys Gln His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly 85 90 95
- Tyr Val Gln Glu Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys
 100 105 110
- Thr Arg Ala Glu Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile 115 120 125
- Glu Leu Lys Gly Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His 130 135 140
- Lys Leu Glu Tyr Asn Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp 145 150 155 160
- Lys Gln Lys Asn Gly Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile 165 170 175
- Glu Asp Gly Ser Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro 180 185 190
- Ile Gly Asp Gly Pro Val Leu Leu Pro Asp Asn His Tyr Leu Ser Thr 195 200 205
- Gln Ser Ala Leu Ser Lys Asp Pro Asn Glu Lys Arg Asp His Met Val

210 215 220 Leu Leu Glu Phe Val Thr Ala Ala Gly Ile Thr His Gly Met Asp Glu 230 Leu Tyr Lys <210> 77 <211> 732 <212> DNA <213> Artificial Sequence <220> <223> Description of Artificial Sequence: Phe(TTC)5GFP <220> <221> CDS <222> (1)..(732) <400> 77 atg ttc ttc ttc ttc agc aag ggc gag gaa ctg ttc act ggc gtg Met Phe Phe Phe Phe Ser Lys Gly Glu Glu Leu Phe Thr Gly Val gtc cca att ctc gtg gaa ctg gat ggc gat gtg aat ggg cac aaa ttt 96 Val Pro Ile Leu Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe 20 tet gte age gga gag ggt gaa ggt gat gee aca tae gga aag ete ace 144 Ser Val Ser Gly Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr ctg aaa ttc atc tgc acc act gga aag ctc cct gtg cca tgg cca aca 192 Leu Lys Phe Ile Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr 55 ctg gtc act acc ttc tct tat ggc gtg cag tgc ttt tcc aga tac cca 240 Leu Val Thr Thr Phe Ser Tyr Gly Val Gln Cys Phe Ser Arg Tyr Pro gac cat atg aag cag cat gac ttt ttc aag agc gcc atg ccc gag ggc 288 Asp His Met Lys Gln His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly 85 90

tat Tyr	gtg Val	cag Gln	gag Glu 100	aga Arg	acc Thr	atc Ile	ttt Phe	ttc Phe 105	aaa Lys	gat Asp	gac Asp	ggg Gly	aac Asn 110	tac Tyr	aag Lys	336
acc Thr	cgc Arg	gct Ala 115	gaa Glu	gtc Val	aag Lys	ttc Phe	gaa Glu 120	ggt Gly	gac Asp	acc Thr	ctg Leu	gtg Val 125	aat Asn	aga Arg	atc Ile	384
gag Glu	ctg Leu 130	aag Lys	ggc Gly	att Ile	gac Asp	ttt Phe 135	aag Lys	gag Glu	gat Asp	gga Gly	aac Asn 140	att Ile	ctc Leu	ggc Gly	cac His	432
aag Lys 145	ctg Leu	gaa Glu	tac Tyr	aac Asn	tat Tyr 150	aac Asn	tcc Ser	cac His	aat Asn	gtg Val 155	tac Tyr	atc Ile	atg Met	gcc Ala	gac Asp 160	480
aag Lys	caa Gln	aag Lys	aat Asn	ggc Gly 165	atc Ile	aag Lys	gtc Val	aac Asn	ttc Phe 170	aag Lys	atc Ile	aga Arg	cac His	aac Asn 175	att Ile	528
gag Glu	gat Asp	gga Gly	tcc Ser 180	gtg Val	cag Gln	ctg Leu	gcc Ala	gac Asp 185	cat His	tat Tyr	caa Gln	cag Gln	aac Asn 190	act Thr	cca Pro	576
atc Ile	ggc Gly	gac Asp 195	ggc Gly	cct Pro	gtg Val	ctc Leu	ctc Leu 200	cca Pro	gac Asp	aac Asn	cat His	tac Tyr 205	ctg Leu	tcc Ser	acc Thr	624
cag Gln	tct Ser 210	gcc Ala	ctg Leu	tct Ser	aaa Lys	gat Asp 215	ccc Pro	aac Asn	gaa Glu	aag Lys	aga Arg 220	gac Asp	cac His	atg Met	gtc Val	672
ctg Leu 225	ctg Leu	gag Glu	ttt Phe	gtg Val	acc Thr 230	gct Ala	gct Ala	Gly ggg	atc Ile	aca Thr 235	cat His	ggc Gly	atg Met	gac Asp	gag Glu 240	720
	tac Tyr	-	tga													732

<210> 78 <211> 243 <212> PRT <213> Artificial Sequence

<400> 78 Met Phe Phe Phe Phe Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr Phe Ser Tyr Gly Val Gln Cys Phe Ser Arg Tyr Pro Asp His Met Lys Gln His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile 115 Glu Leu Lys Gly Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His 130 Lys Leu Glu Tyr Asn Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp Lys Gln Lys Asn Gly Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile 165 170 Glu Asp Gly Ser Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro 185 Ile Gly Asp Gly Pro Val Leu Leu Pro Asp Asn His Tyr Leu Ser Thr Gln Ser Ala Leu Ser Lys Asp Pro Asn Glu Lys Arg Asp His Met Val 215 Leu Leu Glu Phe Val Thr Ala Ala Gly Ile Thr His Gly Met Asp Glu 235

Leu Tyr Lys

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<210> 79
<211> 732
<212> DNA
<213> Artificial Sequence
<220>
<223> Description of Artificial Sequence: Pro(CCC) 5GFP
<220>
<221> CDS
<222> (1)..(732)
<400> 79
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                                                                   48
Met Pro Pro Pro Pro Ser Lys Gly Glu Glu Leu Phe Thr Gly Val
gtc cca att ctc gtg gaa ctg gat ggc gat gtg aat ggg cac aaa ttt
                                                                   96
Val Pro Ile Leu Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe
             20
tet gte age gga gag ggt gaa ggt gat gee aca tae gga aag ete ace
                                                                   144
Ser Val Ser Gly Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr
         35
                             40
ctg aaa ttc atc tgc acc act gga aag ctc cct gtg cca tgg cca aca
                                                                   192
Leu Lys Phe Ile Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr
                         55
ctg gtc act acc ttc tct tat ggc gtg cag tqc ttt tcc aga tac cca
                                                                   240
Leu Val Thr Thr Phe Ser Tyr Gly Val Gln Cys Phe Ser Arg Tyr Pro
                                          75
gac cat atg aag cag cat gac ttt ttc aag agc gcc atg ccc gag ggc
                                                                   288
Asp His Met Lys Gln His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly
tat gtg cag gag aga acc atc ttt ttc aaa gat gac ggg aac tac aag
                                                                   336
Tyr Val Gln Glu Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys
                                105
                                                    110
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acc Thr	cgc Arg	gct Ala 115	gaa Glu	gtc Val	aag Lys	ttc Phe	gaa Glu 120	ggt Gly	gac Asp	acc Thr	ctg Leu	gtg Val 125	aat Asn	aga Arg	atc Ile	384
gag Glu	ctg Leu 130	aag Lys	ggc Gly	att Ile	gac Asp	ttt Phe 135	aag Lys	gag Glu	gat Asp	gga Gly	aac Asn 140	att Ile	ctc Leu	ggc Gly	cac His	432
aag Lys 145	ctg Leu	gaa Glu	tac Tyr	aac Asn	tat Tyr 150	aac Asn	tcc Ser	cac His	aat Asn	gtg Val 155	tac Tyr	atc Ile	atg Met	gcc Ala	gac Asp 160	480
aag Lys	caa Gln	aag Lys	aat Asn	ggc Gly 165	atc Ile	aag Lys	gtc Val	aac Asn	ttc Phe 170	aag Lys	atc Ile	aga Arg	cac His	aac Asn 175	att Ile	528
gag Glu	gat Asp	gga Gly	tcc Ser 180	gtg Val	cag Gln	ctg Leu	gcc Ala	gac Asp 185	cat His	tat Tyr	caa Gln	cag Gln	aac Asn 190	act Thr	cca Pro	576
atc Ile	ggc Gly	gac Asp 195	ggc Gly	cct Pro	gtg Val	ctc Leu	ctc Leu 200	cca Pro	gac Asp	aac Asn	cat His	tac Tyr 205	ctg Leu	tcc Ser	acc Thr	624
cag Gln	tct Ser 210	gcc Ala	ctg Leu	tct Ser	aaa Lys	gat Asp 215	ccc Pro	aac Asn	gaa Glu	aag Lys	aga Arg 220	gac Asp	cac His	atg Met	gtc Val	672
ctg Leu 225	ctg Leu	gag Glu	ttt Phe	gtg Val	acc Thr 230	gct Ala	gct Ala	Gly	atc Ile	aca Thr 235	cat His	ggc Gly	atg Met	gac Asp	gag Glu 240	720
	tac Tyr	aag Lys	tga													732
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Val Pro Ile Leu Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr Phe Ser Tyr Gly Val Gln Cys Phe Ser Arg Tyr Pro Asp His Met Lys Gln His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His 135 Lys Leu Glu Tyr Asn Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp 150 Lys Gln Lys Asn Gly Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile 165 170 Glu Asp Gly Ser Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro 185 Ile Gly Asp Gly Pro Val Leu Leu Pro Asp Asn His Tyr Leu Ser Thr 200 Gln Ser Ala Leu Ser Lys Asp Pro Asn Glu Lys Arg Asp His Met Val 215

Leu Leu Glu Phe Val Thr Ala Ala Gly Ile Thr His Gly Met Asp Glu

Leu Tyr Lys

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<211> 732
<212> DNA
<213> Artificial Sequence
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<221> CDS
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gtc cca att ctc gtg gaa ctg gat ggc gat gtg aat ggg cac aaa ttt
                                                                   96
Val Pro Ile Leu Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe
tet gte age gga gag ggt gaa ggt gat gee aca tae gga aag ete ace
                                                                   144
Ser Val Ser Gly Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr
ctg aaa ttc atc tgc acc act gga aag ctc cct gtg cca tgg cca aca
                                                                   192
Leu Lys Phe Ile Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr
     50
ctg gtc act acc ttc tct tat ggc gtg cag tgc ttt tcc aga tac cca
                                                                   240
Leu Val Thr Thr Phe Ser Tyr Gly Val Gln Cys Phe Ser Arg Tyr Pro
                     70
gac cat atg aag cag cat gac ttt ttc aag agc gcc atg ccc gag ggc
                                                                   288
Asp His Met Lys Gln His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly
                 85
tat gtg cag gag aga acc atc ttt ttc aaa gat gac ggg aac tac aag
                                                                   336
Tyr Val Gln Glu Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys
            100
                                105
acc cgc gct gaa gtc aag ttc gaa ggt gac acc ctg gtg aat aga atc
                                                                   384
Thr Arg Ala Glu Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile
        115
                            120
                                                125
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	ctg Leu 130															432
	ctg Leu															480
	caa Gln															528
	gat Asp															576
	ggc Gly															624
	tct Ser 210															672
ctg Leu 225	ctg Leu	gag Glu	ttt Phe	gtg Val	acc Thr 230	gct Ala	gct Ala	Gly ggg	atc Ile	aca Thr 235	cat His	ggc Gly	atg Met	gac Asp	gag Glu 240	720
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Val	Pro	Ile	Leu 20	Val	Glu	Leu	Asp	Gly 25	Asp	Val	Asn	Gly	His 30	Lys	Phe	

Ser Val Ser Gly Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr

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Leu	Lys 50	Phe	Ile	Cys	Thr	Thr 55	Gly	Lys	Leu	Pro	Val 60	Pro	Trp	Pro	Thr
Leu 65	Val	Thr	Thr	Phe	Ser 70	Tyr	Gly	Val	Gln	Cys 75	Phe	Ser	Arg	Tyr	Pro 80
Asp	His	Met	Lys	Gln 85	His	Asp	Phe	Phe	Lys 90	Ser	Ala	Met	Pro	Glu 95	Gly
Tyr	Val	Gln	Glu 100	Arg	Thr	Ile	Phe	Phe 105	Lys	Asp	Asp	Gly	Asn 110	Tyr	Lys
Thr	Arg	Ala 115	Glu	Val	Lys	Phe	Glu 120	Gly	Asp	Thr	Leu	Val 125	Asn	Arg	Ile
Glu	Leu 130	Lys	Gly	Ile	Asp	Phe 135	Lys	Glu	Asp	Gly	Asn 140	Ile	Leu	Gly	His
Lys 145	Leu	Glu	Tyr	Asn	Tyr 150	Asn	Ser	His	Asn	Val 155	Tyr	Ile	Met	Ala	Asp 160
Lys	Gln	Lys	Asn	Gly 165	Ile	Lys	Val	Asn	Phe 170	Lys	Ile	Arg	His	Asn 175	Ile
Glu	Asp	Gly	Ser 180	Val	Gln	Leu	Ala	Asp 185	His	Tyr	Gln	Gln	Asn 190	Thr	Pro
Ile	Gly	Asp 195	Gly	Pro	Val	Leu	Leu 200	Pro	Asp	Asn	His	Tyr 205	Leu	Ser	Thr
Gln	Ser 210	Ala	Leu	Ser	Lys	Asp 215	Pro	Asn	Glu	Lys	Arg 220	Asp	His	Met	Val
Leu 225	Leu	Glu	Phe	Val	Thr 230	Ala	Ala	Gly	Ile	Thr 235	His	Gly	Met	Asp	Glu 240
Leu	Tyr	Lys													
<210	1> 85	₹													

<210> 83 <211> 732 <212> DNA <213> Artificial Sequence

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gtc cca att ctc gtg gaa ctg gat ggc gat gtg aat ggg cac aaa ttt
                                                                   96
Val Pro Ile Leu Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe
             20
tet gte age gga gag ggt gaa ggt gat gee aca tae gga aag ete ace
                                                                   144
Ser Val Ser Gly Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr
ctg aaa ttc atc tgc acc act gga aag ctc cct gtg cca tgg cca aca
                                                                   192
Leu Lys Phe Ile Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr
     50
ctg gtc act acc ttc tct tat ggc gtg cag tgc ttt tcc aga tac cca
                                                                   240
Leu Val Thr Thr Phe Ser Tyr Gly Val Gln Cys Phe Ser Arg Tyr Pro
                     70
gac cat atg aag cag cat gac ttt ttc aag agc gcc atg ccc gag ggc
                                                                   288
Asp His Met Lys Gln His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly
                 85
tat gtg cag gag aga acc atc ttt ttc aaa gat gac ggg aac tac aag
                                                                   336
Tyr Val Gln Glu Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys
                                105
acc cgc gct gaa gtc aag ttc gaa ggt gac acc ctg gtg aat aga atc
                                                                   384
Thr Arg Ala Glu Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile
                            120
gag ctg aag ggc att gac ttt aag gag gat gga aac att ctc ggc cac
                                                                   432
Glu Leu Lys Gly Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His
                        135
                                            140
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aag Lys 145	ctg Leu	gaa Glu	tac Tyr	aac Asn	tat Tyr 150	aac Asn	tcc Ser	cac His	aat Asn	gtg Val 155	tac Tyr	atc Ile	atg Met	gcc Ala	gac Asp 160	480
aag Lys	caa Gln	aag Lys	aat Asn	ggc Gly 165	atc Ile	aag Lys	gtc Val	aac Asn	ttc Phe 170	aag Lys	atc Ile	aga Arg	cac His	aac Asn 175	att Ile	528
gag Glu	gat Asp	gga Gly	tcc Ser 180	gtg Val	cag Gln	ctg Leu	gcc Ala	gac Asp 185	cat His	tat Tyr	caa Gln	cag Gln	aac Asn 190	act Thr	cca Pro	576
atc Ile	ggc Gly	gac Asp 195	ggc Gly	cct Pro	gtg Val	ctc Leu	ctc Leu 200	cca Pro	gac Asp	aac Asn	cat His	tac Tyr 205	ctg Leu	tcc Ser	acc Thr	624
cag Gln	tct Ser 210	gcc Ala	ctg Leu	tct Ser	aaa Lys	gat Asp 215	ccc Pro	aac Asn	gaa Glu	aag Lys	aga Arg 220	gac Asp	cac His	atg Met	gtc Val	672
ctg Leu 225	ctg Leu	gag Glu	ttt Phe	gtg Val	acc Thr 230	gct Ala	gct Ala	ggg Gly	atc Ile	aca Thr 235	cat His	ggc Gly	atg Met	gac Asp	gag Glu 240	720
	tac Tyr		tga													732
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Val	Pro	Ile	Leu 20	Val	Glu	Leu	Asp	Gly 25	Asp	Val	Asn	Gly	His 30	Lys	Phe	
Ser	Val	Ser 35	Gly	Glu	Gly	Glu	Gly 40	Asp	Ala	Thr	Tyr	Gly 45	Lys	Leu	Thr	
Leu	Lys 50	Phe	Ile	Cys	Thr	Thr 55	Gly	Lys	Leu	Pro	Val 60	Pro	Trp	Pro	Thr	

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Leu Val Thr Thr Phe Ser Tyr Gly Val Gln Cys Phe Ser Arg Tyr Pro
Asp His Met Lys Gln His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly
Tyr Val Gln Glu Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys
Thr Arg Ala Glu Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile
Glu Leu Lys Gly Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His
    130
Lys Leu Glu Tyr Asn Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp
Lys Gln Lys Asn Gly Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile
                165
Glu Asp Gly Ser Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro
            180
Ile Gly Asp Gly Pro Val Leu Leu Pro Asp Asn His Tyr Leu Ser Thr
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Gln Ser Ala Leu Ser Lys Asp Pro Asn Glu Lys Arg Asp His Met Val

Leu Leu Glu Phe Val Thr Ala Ala Gly Ile Thr His Gly Met Asp Glu

195

Leu Tyr Lys

<210> 85

<211> 732

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Pro(CGA)5GFP

215

230

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aag Lys	caa Gln	aag Lys	aat Asn	ggc Gly 165	atc Ile	aag Lys	gtc Val	aac Asn	ttc Phe 170	aag Lys	atc Ile	aga Arg	cac His	aac Asn 175	att Ile	528
gag Glu	gat Asp	gga Gly	tcc Ser 180	gtg Val	cag Gln	ctg Leu	gcc Ala	gac Asp 185	cat His	tat Tyr	caa Gln	cag Gln	aac Asn 190	act Thr	cca Pro	576
atc Ile	ggc Gly	gac Asp 195	ggc Gly	cct Pro	gtg Val	ctc Leu	ctc Leu 200	cca Pro	gac Asp	aac Asn	cat His	tac Tyr 205	ctg Leu	tcc Ser	acc Thr	624
cag Gln	tct Ser 210	gcc Ala	ctg Leu	tct Ser	aaa Lys	gat Asp 215	ccc Pro	aac Asn	gaa Glu	aag Lys	aga Arg 220	gac Asp	cac His	atg Met	gtc Val	672
ctg Leu 225	ctg Leu	gag Glu	ttt Phe	gtg Val	acc Thr 230	gct Ala	gct Ala	ggg Gly	atc Ile	aca Thr 235	cat His	ggc Gly	atg Met	gac Asp	gag Glu 240	720
	tac Tyr		tga													732
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Val	Pro	Ile	Leu 20	Val	Glu	Leu	Asp	Gly 25	Asp	Val	Asn	Gly	His 30	Lys	Phe	
Ser	Val	Ser 35	Gly	Glu	Gly	Glu	Gly 40	Asp	Ala	Thr	Tyr	Gly 45	Lys	Leu	Thr	
Leu	Lys 50	Phe	Ile	Cys	Thr	Thr 55	Gly	Lys	Leu	Pro	Val 60	Pro	Trp	Pro	Thr	
Leu 65	Val	Thr	Thr	Phe	Ser 70	Tyr	Gly	Val	Gln	Cys 75	Phe	Ser	Arg	Tyr	Pro 80	

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Asp His Met Lys Gln His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly 85

Tyr Val Gln Glu Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys 100
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Thr Arg Ala Glu Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile 115 120 125

Glu Leu Lys Gly Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His 130 135 140

Lys Leu Glu Tyr Asn Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp 150 155 160

Lys Gln Lys Asn Gly Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile 165 170 175

Ile Gly Asp Gly Pro Val Leu Leu Pro Asp Asn His Tyr Leu Ser Thr 195 200 205

Gln Ser Ala Leu Ser Lys Asp Pro Asn Glu Lys Arg Asp His Met Val210 215 220

Leu Leu Glu Phe Val Thr Ala Ala Gly Ile Thr His Gly Met Asp Glu 225 230 235 240

Leu Tyr Lys

<210> 87

<211> 732 <212> DNA

<213> Artificial Sequence

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<223> Description of Artificial Sequence: Ser(AGC)5GFP

<220>

<221> CDS

<222> (1)..(732)

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gtc Val	cca Pro	att Ile	ctc Leu 20	gtg Val	gaa Glu	ctg Leu	gat Asp	ggc Gly 25	gat Asp	gtg Val	aat Asn	ggg Gly	cac His 30	aaa Lys	ttt Phe	96
tct Ser	gtc Val	agc Ser 35	gga Gly	gag Glu	ggt Gly	gaa Glu	ggt Gly 40	gat Asp	gcc Ala	aca Thr	tac Tyr	gga Gly 45	aag Lys	ctc Leu	acc Thr	144
ctg Leu	aaa Lys 50	ttc Phe	atc Ile	tgc Cys	acc Thr	act Thr 55	gga Gly	aag Lys	ctc Leu	cct Pro	gtg Val 60	cca Pro	tgg Trp	cca Pro	aca Thr	192
ctg Leu 65	gtc Val	act Thr	acc Thr	ttc Phe	tct Ser 70	tat Tyr	ggc Gly	gtg Val	cag Gln	tgc Cys 75	ttt Phe	tcc Ser	aga Arg	tac Tyr	cca Pro 80	240
gac Asp	cat His	atg Met	aag Lys	cag Gln 85	cat His	gac Asp	ttt Phe	ttc Phe	aag Lys 90	agc Ser	gcc Ala	atg Met	ccc Pro	gag Glu 95	ggc Gly	288
tat Tyr	gtg Val	cag Gln	gag Glu 100	aga Arg	acc Thr	atc Ile	ttt Phe	ttc Phe 105	aaa Lys	gat Asp	gac Asp	Glà ààà	aac Asn 110	tac Tyr	aag Lys	336
acc Thr	cgc Arg	gct Ala 115	gaa Glu	gtc Val	aag Lys	ttc Phe	gaa Glu 120	ggt Gly	gac Asp	acc Thr	ctg Leu	gtg Val 125	aat Asn	aga Arg	atc Ile	384
gag Glu	ctg Leu 130	aag Lys	ggc Gly	att Ile	gac Asp	ttt Phe 135	aag Lys	gag Glu	gat Asp	gga Gly	aac Asn 140	att Ile	ctc Leu	ggc Gly	cac His	432
aag Lys 145	ctg Leu	gaa Glu	tac Tyr	aac Asn	tat Tyr 150	aac Asn	tcc Ser	cac His	aat Asn	gtg Val 155	tac Tyr	atc Ile	atg Met	gcc Ala	gac Asp 160	480
aag Lys	caa Gln	aag Lys	aat Asn	ggc Gly 165	atc Ile	aag Lys	gtc Val	aac Asn	ttc Phe 170	aag Lys	atc Ile	aga Arg	cac His	aac Asn 175	att Ile	528

gag Glu	gat Asp	gga Gly	tcc Ser 180	gtg Val	cag Gln	ctg Leu	gcc Ala	gac Asp 185	cat His	tat Tyr	caa Gln	cag Gln	aac Asn 190	act Thr	cca Pro	576
atc Ile	ggc Gly	gac Asp 195	ggc Gly	cct Pro	gtg Val	ctc Leu	ctc Leu 200	cca Pro	gac Asp	aac Asn	cat His	tac Tyr 205	ctg Leu	tcc Ser	acc Thr	624
cag Gln	tct Ser 210	gcc Ala	ctg Leu	tct Ser	aaa Lys	gat Asp 215	ccc Pro	aac Asn	gaa Glu	aag Lys	aga Arg 220	gac Asp	cac His	atg Met	gtc Val	672
ctg Leu 225	ctg Leu	gag Glu	ttt Phe	gtg Val	acc Thr 230	gct Ala	gct Ala	ggg Gly	atc Ile	aca Thr 235	cat His	ggc Gly	atg Met	gac Asp	gag Glu 240	720
_	tac Tyr	_	tga													732

<210> 88 <211> 243 <212> PRT

<213> Artificial Sequence

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Ser Val Ser Gly Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr 35 40 45

Leu Lys Phe Ile Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr 50 55 60

Leu Val Thr Thr Phe Ser Tyr Gly Val Gln Cys Phe Ser Arg Tyr Pro 65 70 75 80

Asp His Met Lys Gln His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly 85 90 95

Tyr Val Gln Glu Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys

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100
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Thr Arg Ala Glu Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile
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Glu Leu Lys Gly Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His
Lys Leu Glu Tyr Asn Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp
Lys Gln Lys Asn Gly Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile
Glu Asp Gly Ser Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro
Ile Gly Asp Gly Pro Val Leu Leu Pro Asp Asn His Tyr Leu Ser Thr
Gln Ser Ala Leu Ser Lys Asp Pro Asn Glu Lys Arg Asp His Met Val
Leu Leu Glu Phe Val Thr Ala Ala Gly Ile Thr His Gly Met Asp Glu
225
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Leu Tyr Lys
<210> 89
<211> 732
<212> DNA
<213> Artificial Sequence
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<222> (1)..(732)
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                                                         15
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Val	Pro	Ile	Leu 20	Val	Glu	Leu	Āsp	Gly 25	Āsp	Ϋaĺ	Asn	ĞÎÿ	His 30	Lys	Phe	
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ctg Leu	aaa Lys 50	ttc Phe	atc Ile	tgc Cys	acc Thr	act Thr 55	gga Gly	aag Lys	ctc Leu	cct Pro	gtg Val 60	cca Pro	tgg Trp	cca Pro	aca Thr	192
ctg Leu 65	gtc Val	act Thr	acc Thr	ttc Phe	tct Ser 70	tat Tyr	ggc Gly	gtg Val	cag Gln	tgc Cys 75	ttt Phe	tcc Ser	aga Arg	tac Tyr	cca Pro 80	240
Asp	cat His	Met	Lys	Gln 85	His	Asp	Phe	Phe	Lys 90	Ser	Ala	Met	Pro	Glu 95	Gly	288
Tyr	gtg Val	G⊥n	Glu 100	Arg	Thr	Ile	Phe	Phe 105	Lys	Asp	Asp	Gly	Asn 110	Tyr	Lys	336
acc Thr	cgc Arg	gct Ala 115	gaa Glu	gtc Val	aag Lys	ttc Phe	gaa Glu 120	ggt Gly	gac Asp	acc Thr	ctg Leu	gtg Val 125	aat Asn	aga Arg	atc Ile	384
gag Glu	ctg Leu 130	aag Lys	ggc Gly	att Ile	gac Asp	ttt Phe 135	aag Lys	gag Glu	gat Asp	gga Gly	aac Asn 140	att Ile	ctc Leu	ggc Gly	cac His	432
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Thr Arg Ala Glu Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile

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Ile Gly Asp Gly Pro Val Leu Leu Pro Asp Asn His Tyr Leu Ser Thr
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Leu Val Thr Thr Phe Ser Tyr Gly Val Gln Cys Phe Ser Arg Tyr Pro 65 70 75 80

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Lys Gln Lys Asn Gly Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile 165 170 175

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acc Thr	cgc Arg	gct Ala 115	gaa Glu	gtc Val	aag Lys	ttc Phe	gaa Glu 120	ggt Gly	gac Asp	acc Thr	ctg Leu	gtg Val 125	aat Asn	aga Arg	atc Ile	384
gag Glu	ctg Leu 130	aag Lys	ggc Gly	att Ile	gac Asp	ttt Phe 135	aag Lys	gag Glu	gat Asp	gga Gly	aac Asn 140	att Ile	ctc Leu	ggc Gly	cac His	432
aag Lys 145	ctg Leu	gaa Glu	tac Tyr	aac Asn	tat Tyr 150	aac Asn	tcc Ser	cac His	aat Asn	gtg Val 155	tac Tyr	atc Ile	atg Met	gcc Ala	gac Asp 160	480
aag Lys	caa Gln	aag Lys	aat Asn	ggc Gly 165	atc Ile	aag Lys	gtc Val	aac Asn	ttc Phe 170	aag Lys	atc Ile	aga Arg	cac His	aac Asn 175	att Ile	528
gag Glu	gat Asp	gga Gly	tcc Ser 180	gtg Val	cag Gln	ctg Leu	gcc Ala	gac Asp 185	cat His	tat Tyr	caa Gln	cag Gln	aac Asn 190	act Thr	cca Pro	576
atc Ile	ggc Gly	gac Asp 195	Gly	cct Pro	gtg Val	ctc Leu	ctc Leu 200	cca Pro	gac Asp	aac Asn	cat His	tac Tyr 205	ctg Leu	tcc Ser	acc Thr	624
cag Gln	tct Ser 210	gcc Ala	ctg Leu	tct Ser	aaa Lys	gat Asp 215	ccc Pro	aac Asn	gaa Glu	aag Lys	aga Arg 220	gac Asp	cac His	atg Met	gtc Val	672
ctg Leu 225	Leu	gag Glu	ttt Phe	gtg Val	acc Thr 230	gct Ala	gct Ala	ggg	atc Ile	aca Thr 235	His	ggc Gly	atg Met	gac Asp	gag Glu 240	720
	tac Tyr															732

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Leu Tyr Lys													
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		gat gcc aca tac gga 7 Asp Ala Thr Tyr Gly 1 45											
		a aag ctc cct gtg cca 7 Lys Leu Pro Val Pro 60											
		e gtg cag tgc ttt tcc y Val Gln Cys Phe Ser 75											
		t ttc aag agc gcc atg e Phe Lys Ser Ala Met 90											
		t ttc aaa gat gac ggg e Phe Lys Asp Asp Gly 105											

					aag Lys											384
gag Glu	ctg Leu 130	aag Lys	ggc Gly	att Ile	gac Asp	ttt Phe 135	aag Lys	gag Glu	gat Asp	gga Gly	aac Asn 140	att Ile	ctc Leu	ggc Gly	cac His	432
					tat Tyr 150											480
					atc Ile											528
					cag Gln											576
					gtg Val											624
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					acc Thr 230											720
_	tac Tyr	_	tga													732
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Val Pro Ile Leu Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr Phe Ser Tyr Gly Val Gln Cys Phe Ser Arg Tyr Pro Asp His Met Lys Gln His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His 135 Lys Leu Glu Tyr Asn Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp Lys Gln Lys Asn Gly Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile 165 Glu Asp Gly Ser Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro 185 Ile Gly Asp Gly Pro Val Leu Leu Pro Asp Asn His Tyr Leu Ser Thr 200 Gln Ser Ala Leu Ser Lys Asp Pro Asn Glu Lys Arg Asp His Met Val 210 215 Leu Leu Glu Phe Val Thr Ala Ala Gly Ile Thr His Gly Met Asp Glu

230

Leu Tyr Lys

-cxlix-

235

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Val Pro Ile Leu Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe
             20
tct gtc agc gga gag ggt gaa ggt gat gcc aca tac gga aag ctc acc
                                                                   144
Ser Val Ser Gly Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr
ctg aaa ttc atc tgc acc act gga aag ctc cct gtg cca tgg cca aca
                                                                   192
Leu Lys Phe Ile Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr
     50
ctg gtc act acc ttc tct tat ggc gtg cag tgc ttt tcc aga tac cca
Leu Val Thr Thr Phe Ser Tyr Gly Val Gln Cys Phe Ser Arg Tyr Pro
 65
                     70
                                                              80
                                          7.5
gac cat atg aag cag cat gac ttt ttc aag agc gcc atg ccc gag ggc
                                                                   288
Asp His Met Lys Gln His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly
                 85
                                      90
                                                          95
tat gtg cag gag aga acc atc ttt ttc aaa gat gac ggg aac tac aag
Tyr Val Gln Glu Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys
            100
                                105
                                                     110
acc ege get gaa gte aag tte gaa ggt gae acc etg gtg aat aga ate
Thr Arg Ala Glu Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile
        115
                            120
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		aag Lys														432
GIU	130	цуо	Фту	110	1100	135	дуо	Oiu	1150	Ory	140	110	LCu	CTY	1110	
		gaa Glu														480
		aag Lys														528
		gga Gly														576
		gac Asp 195							_				_			624
		gcc Ala	_			_			_	_	_	_		_	_	672
		gag Glu														720
~	tac Tyr	aag Lys	tga													732
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Val	Pro	Ile	Leu 20	Val	Glu	Leu	Asp	Gly 25	Asp	Val	Asn	Gly	His 30	Lys	Phe	

Ser Val Ser Gly Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr 35 40 45

Leu Lys Phe Ile Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr 50 55 60

Leu Val Thr Thr Phe Ser Tyr Gly Val Gln Cys Phe Ser Arg Tyr Pro 65 70 75 80

Asp His Met Lys Gln His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly 85 90 95

Tyr Val Gln Glu Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys $100 \hspace{1.5cm} 105 \hspace{1.5cm} 110 \hspace{1.5cm}$

Thr Arg Ala Glu Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile 115 120 125

Glu Leu Lys Gly Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His 130 135

Lys Leu Glu Tyr Asn Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp 145 150 155 160

Lys Gln Lys Asn Gly Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile 165 170 175

Glu Asp Gly Ser Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro 180 185 190

Ile Gly Asp Gly Pro Val Leu Leu Pro Asp Asn His Tyr Leu Ser Thr 195 200 205

Gln Ser Ala Leu Ser Lys Asp Pro Asn Glu Lys Arg Asp His Met Val 210 215 220

Leu Leu Glu Phe Val Thr Ala Ala Gly Ile Thr His Gly Met Asp Glu 225 230 235 240

Leu Tyr Lys

<210> 105

<211> 732

<212> DNA

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				gtg Val											96
				gag Glu											144
				tgc Cys											192
				ttc Phe											240
				cag Gln 85											288
				aga Arg											336
				gtc Val											384
				att Ile											432

	Leu															480
	caa Gln															528
	gat Asp															576
	ggc Gly															624
	tct Ser 210															672
	ctg Leu															720
-	tac Tyr	_	tga													732
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Val	Pro	Ile	Leu 20	Val	Glu	Leu	Asp	Gly 25	Asp	Val	Asn	Gly	His 30	Lys	Phe	
Ser	Val	Ser 35	Gly	Glu	Gly	Glu	Gly 40	Asp	Ala	Thr	Tyr	Gly 45	Lys	Leu	Thr	
Leu	Lys	Phe	Ile	Cys	Thr	Thr	Glv	Lvs	Leu	Pro	Va]	Pro	Trp	Pro	Thr	

	50					55					60				
Leu 65	Val	Thr	Thr	Phe	Ser 70	Tyr	Gly	Val	Gln	Cys 75	Phe	Ser	Arg	Tyr	Pro 80
Asp	His	Met	Lys	Gln 85	His	Asp	Phe	Phe	Lys 90	Ser	Ala	Met	Pro	Glu 95	Gly
Tyr	Val	Gln	Glu 100	Arg	Thr	Ile	Phe	Phe 105	Lys	Asp	Asp	Gly	Asn 110	Tyr	Lys
Thr	Arg	Ala 115	Glu	Val	Lys	Phe	Glu 120	Gly	Asp	Thr	Leu	Val 125	Asn	Arg	Ile
Glu	Leu 130	Lys	Gly	Ile	Asp	Phe 135	Lys	Glu	Asp	Gly	Asn 140	Ile	Leu	Gly	His
Lys 145	Leu	Glu	Tyr	Asn	Tyr 150	Asn	Ser	His	Asn	Val 155	Tyr	Ile	Met	Ala	Asp 160
Lys	Gln	Lys	Asn	Gly 165	Ile	Lys	Val	Asn	Phe 170	Lys	Ile	Arg	His	Asn 175	Ile
Glu	Asp	Gly	Ser 180	Val	Gln	Leu	Ala	Asp 185	His	Tyr	Gln	Gln	Asn 190	Thr	Pro
Ile	Gly	Asp 195	Gly	Pro	Val	Leu	Leu 200	Pro	Asp	Asn	His	Tyr 205	Leu	Ser	Thr
Gln	Ser 210	Ala	Leu	Ser	Lys	Asp 215	Pro	Asn	Glu	Lys	Arg 220	Asp	His	Met	Val
Leu 225	Leu	Glu	Phe	Val	Thr 230	Ala	Ala	Gly	Ile	Thr 235	His	Gly	Met	Asp	Glu 240
Leu	Tyr	Lys													
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	Gln															528
	gat Asp															576
	ggc Gly															624
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_	tac Tyr	_	tga													732
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Val	Pro	Ile	Leu 20	Val	Glu	Leu	Asp	Gly 25	Asp	Val	Asn	Gly	His 30	Lys	Phe	
Ser	Val	Ser 35	Gly	Glu	Gly	Glu	Gly 40	Asp	Ala	Thr	Tyr	Gly 45	Lys	Leu	Thr	
Leu	Lys 50	Phe	Ile	Cys	Thr	Thr 55	Gly	Lys	Leu	Pro	Val 60	Pro	Trp	Pro	Thr	
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<222> (1)..(732)

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Thr Arg Ala Glu Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile
Glu Leu Lys Gly Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His
Lys Leu Glu Tyr Asn Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp
                    150
Lys Gln Lys Asn Gly Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile
Glu Asp Gly Ser Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro
Ile Gly Asp Gly Pro Val Leu Leu Pro Asp Asn His Tyr Leu Ser Thr
Gln Ser Ala Leu Ser Lys Asp Pro Asn Glu Lys Arg Asp His Met Val
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Leu Leu Glu Phe Val Thr Ala Ala Gly Ile Thr His Gly Met Asp Glu
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Leu Tyr Lys
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			gga Gly													144
ctg Leu	aaa Lys 50	ttc Phe	atc Ile	tgc Cys	acc Thr	act Thr 55	gga Gly	aag Lys	ctc Leu	cct Pro	gtg Val 60	cca Pro	tgg Trp	cca Pro	aca Thr	192
ctg Leu 65	gtc Val	act Thr	acc Thr	ttc Phe	tct Ser 70	tat Tyr	ggc Gly	gtg Val	cag Gln	tgc Cys 75	ttt Phe	tcc Ser	aga Arg	tac Tyr	cca Pro 80	240
			aag Lys													288
tat Tyr	gtg Val	cag Gln	gag Glu 100	aga Arg	acc Thr	atc Ile	ttt Phe	ttc Phe 105	aaa Lys	gat Asp	gac Asp	Gly ggg	aac Asn 110	tac Tyr	aag Lys	336
acc Thr	cgc Arg	gct Ala 115	gaa Glu	gtc Val	aag Lys	ttc Phe	gaa Glu 120	ggt Gly	gac Asp	acc Thr	ctg Leu	gtg Val 125	aat Asn	aga Arg	atc Ile	384
gag Glu	ctg Leu 130	aag Lys	ggc Gly	att Ile	gac Asp	ttt Phe 135	aag Lys	gag Glu	gat Asp	gga Gly	aac Asn 140	att Ile	ctc Leu	ggc Gly	cac His	432
aag Lys 145	ctg Leu	gaa Glu	tac Tyr	aac Asn	tat Tyr 150	aac Asn	tcc Ser	cac His	aat Asn	gtg Val 155	tac Tyr	atc Ile	atg Met	gcc Ala	gac Asp 160	480
aag Lys	caa Gln	aag Lys	aat Asn	ggc Gly 165	atc Ile	aag Lys	gtc Val	aac Asn	ttc Phe 170	aag Lys	atc Ile	aga Arg	cac His	aac Asn 175	att Ile	528

		gga Gly														576
		gac Asp 195														624
		gcc Ala														672
ctg Leu 225	ctg Leu	gag Glu	ttt Phe	gtg Val	acc Thr 230	gct Ala	gct Ala	Gly Ggg	atc Ile	aca Thr 235	cat His	ggc Gly	atg Met	gac Asp	gag Glu 240	720
	tac Tyr	aag Lys	tga													732
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Val	Pro	Ile	Leu 20	Val	Glu	Leu	Asp	Gly 25	Asp	Val	Asn	Gly	His 30	Lys	Phe	
Ser	Val	Ser 35	Gly	Glu	Gly	Glu	Gly 40	Asp	Ala	Thr	Tyr	Gly 45	Lys	Leu	Thr	
Leu	Lys 50	Phe	Ile	Cys	Thr	Thr 55	Gly	Lys	Leu	Pro	Val 60	Pro	Trp	Pro	Thr	
Leu 65	Val	Thr	Thr	Phe	Ser 70	Tyr	Gly	Val	Gln	Cys 75	Phe	Ser	Arg	Tyr	Pro 80	
Asp	His	Met	Lys	Gln 85	His	Asp	Phe	Phe	Lys 90	Ser	Ala	Met	Pro	Glu 95	Gly	

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Tyr Val Gln Glu Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys
                                105
Thr Arg Ala Glu Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile
Glu Leu Lys Gly Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His
Lys Leu Glu Tyr Asn Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp
145
Lys Gln Lys Asn Gly Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile
Glu Asp Gly Ser Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro
Ile Gly Asp Gly Pro Val Leu Leu Pro Asp Asn His Tyr Leu Ser Thr
Gln Ser Ala Leu Ser Lys Asp Pro Asn Glu Lys Arg Asp His Met Val
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                        215
Leu Leu Glu Phe Val Thr Ala Ala Gly Ile Thr His Gly Met Asp Glu
225
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Leu Tyr Lys
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	cca Pro															96
	gtc Val															144
	aaa Lys 50															192
	gtc Val															240
	cat His															288
	gtg Val															336
	cgc Arg															384
	ctg Leu 130															432
	ctg Leu															480
	caa Gln															528
gag Glu	gat Asp	gga Gly	tcc Ser 180	gtg Val	cag Gln	ctg Leu	gcc Ala	gac Asp 185	cat His	tat Tyr	caa Gln	cag Gln	aac Asn 190	act Thr	cca Pro	576

					ctc Leu									624
_		_	-		gat Asp 215		_	_	_	_		_	_	672
_	_				gct Ala	_					_	_		720
_	tac Tyr	aag Lys	tga											732
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<213> Artificial Sequence

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Ser Val Ser Gly Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr 35 40 45

Leu Lys Phe Ile Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr 50 55 60

Leu Val Thr Thr Phe Ser Tyr Gly Val Gln Cys Phe Ser Arg Tyr Pro 65 70 75 80

Asp His Met Lys Gln His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly 85 90 95

Tyr Val Gln Glu Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys 100 105 110

Thr Arg Ala Glu Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile

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115
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                                                125
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                        135
Lys Leu Glu Tyr Asn Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp
145
Lys Gln Lys Asn Gly Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile
Glu Asp Gly Ser Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro
Ile Gly Asp Gly Pro Val Leu Leu Pro Asp Asn His Tyr Leu Ser Thr
Gln Ser Ala Leu Ser Lys Asp Pro Asn Glu Lys Arg Asp His Met Val
Leu Leu Glu Phe Val Thr Ala Ala Gly Ile Thr His Gly Met Asp Glu
225
                    230
Leu Tyr Lys
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                                     10
gtc cca att ctc gtg gaa ctg gat ggc gat gtg aat ggg cac aaa ttt
                                                                  96
Val Pro Ile Leu Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe
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			cct gtg cca tgg Pro Val Pro Trp 60	
			tgc ttt tcc aga Cys Phe Ser Arg 75	
			age gee atg eed Ser Ala Met Pro	
	Arg Thr Ile		gat gac ggg aac Asp Asp Gly Asr 110	Tyr Lys
	_		acc ctg gtg aat Thr Leu Val Asr 125	9
			gga aac att ctc Gly Asn Ile Leu 140	
			gtg tac atc atc Val Tyr Ile Met 155	
		-	aag atc aga cac Lys Ile Arg His	
	Val Gln Leu		tat caa cag aad Tyr Gln Gln Asr 190	n Thr Pro
			aac cat tac cto Asn His Tyr Let 205	

cag tct gcc Gln Ser Ala 210					Lys						672
ctg ctg gag Leu Leu Glu 225											720
ctg tac aag Leu Tyr Lys	tga										732
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Val Pro Ile	Leu Val 20	Glu Leu	_	y Asp 25	Val	Asn	Gly	His 30	Lys	Phe	
Ser Val Ser 35	Gly Glu	Gly Glu	Gly As	sp Ala	Thr	Tyr	Gly 45	Lys	Leu	Thr	
Leu Lys Phe 50	Ile Cys	Thr Thr 55	Gly Ly	ys Leu	Pro	Val 60	Pro	Trp	Pro	Thr	
Leu Val Thr 65	Thr Phe	Ser Tyr 70	Gly Va	al Gln	Cys 75	Phe	Ser	Arg	Tyr	Pro 80	
Asp His Met	Lys Gln 85	His Asp	Phe Ph	ne Lys 90	Ser	Ala	Met	Pro	Glu 95	Gly	
Tyr Val Gln	Glu Arg 100	Thr Ile	Phe Ph		Asp	Asp	Gly	Asn 110	Tyr	Lys	
Thr Arg Ala 115	Glu Val	Lys Phe	Glu Gl 120	Ly Asp	Thr	Leu	Val 125	Asn	Arg	Ile	

Glu Leu Lys Gly Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His 130 $$ 135 $$ 140

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Lys Leu Glu Tyr Asn Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp
145
Lys Gln Lys Asn Gly Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile
Glu Asp Gly Ser Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro
Ile Gly Asp Gly Pro Val Leu Leu Pro Asp Asn His Tyr Leu Ser Thr
Gln Ser Ala Leu Ser Lys Asp Pro Asn Glu Lys Arg Asp His Met Val
Leu Leu Glu Phe Val Thr Ala Ala Gly Ile Thr His Gly Met Asp Glu
                     230
Leu Tyr Lys
<210> 115
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<223> Description of Artificial Sequence: Val(GTC)5GFP
<220>
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<222> (1)..(732)
<400> 115
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gtc cca att ctc gtg gaa ctg gat ggc gat gtg aat ggg cac aaa ttt
                                                                       96
Val Pro Ile Leu Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe
              20
                                   25
tet gte age gga gag ggt gaa ggt gat gee aca tae gga aag ete ace
Ser Val Ser Gly Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr
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	35	ō				40					45				
Leu L	aa tto ys Phe 50														192
ctg gt Leu Va 65	tc act	t acc r Thr	ttc Phe	tct Ser 70	tat Tyr	ggc Gly	gtg Val	cag Gln	tgc Cys 75	ttt Phe	tcc Ser	aga Arg	tac Tyr	cca Pro 80	240
gac ca Asp H:															288
tat gi Tyr Va	tg caq al Glr	g gag n Glu 100	aga Arg	acc Thr	atc Ile	ttt Phe	ttc Phe 105	aaa Lys	gat Asp	gac Asp	ggg Gly	aac Asn 110	tac Tyr	aag Lys	336
acc co	gc gct rg Ala 115	a Glu	gtc Val	aag Lys	ttc Phe	gaa Glu 120	ggt Gly	gac Asp	acc Thr	ctg Leu	gtg Val 125	aat Asn	aga Arg	atc Ile	384
gag ct Glu Le 13	tg aaq eu Lys 30	g ggc s Gly	att Ile	gac Asp	ttt Phe 135	aag Lys	gag Glu	gat Asp	gga Gly	aac Asn 140	att Ile	ctc Leu	ggc Gly	cac His	432
aag ct Lys Le 145	tg gaa eu Gli	a tac ı Tyr	aac Asn	tat Tyr 150	aac Asn	tcc Ser	cac His	aat Asn	gtg Val 155	tac Tyr	atc Ile	atg Met	gcc Ala	gac Asp 160	480
aag ca Lys G	aa aaq ln Lys	g aat s Asn	ggc Gly 165	atc Ile	aag Lys	gtc Val	aac Asn	ttc Phe 170	aag Lys	atc Ile	aga Arg	cac His	aac Asn 175	att Ile	528
gag ga Glu As	at gga sp Gly	a tcc y Ser 180	gtg Val	cag Gln	ctg Leu	gcc Ala	gac Asp 185	cat His	tat Tyr	caa Gln	cag Gln	aac Asn 190	act Thr	cca Pro	576
atc go Ile G	gc gad ly Asp 195	Gly	cct Pro	gtg Val	ctc Leu	ctc Leu 200	cca Pro	gac Asp	aac Asn	cat His	tac Tyr 205	ctg Leu	tcc Ser	acc Thr	624
cag to Gln Se 21	ct gcd er Ala 10	c ctg a Leu	tct Ser	aaa Lys	gat Asp 215	ccc Pro	aac Asn	gaa Glu	aag Lys	aga Arg 220	gac Asp	cac His	atg Met	gtc Val	672

	tg gag eu Glu														720
	ac aag yr Lys	tga													732
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Val P	ro Ile	Leu 20	Val	Glu	Leu	Asp	Gly 25	Asp	Val	Asn	Gly	His 30	Lys	Phe	
Ser V	al Ser 35	_	Glu	Gly	Glu	Gly 40	Asp	Ala	Thr	Tyr	Gly 45	Lys	Leu	Thr	
Leu L	ys Phe 50	Ile	Cys	Thr	Thr 55	Gly	Lys	Leu	Pro	Val 60	Pro	Trp	Pro	Thr	
Leu V 65	al Thr	Thr	Phe	Ser 70	Tyr	Gly	Val	Gln	Cys 75	Phe	Ser	Arg	Tyr	Pro 80	
Asp H	lis Met	Lys	Gln 85	His	Asp	Phe	Phe	Lys 90	Ser	Ala	Met	Pro	Glu 95	Gly	
Tyr V	al Gln	Glu 100	Arg	Thr	Ile	Phe	Phe 105	Lys	Asp	Asp	Gly	Asn 110	Tyr	Lys	
Thr A	rg Ala 115		Val	Lys	Phe	Glu 120	Gly	Asp	Thr	Leu	Val 125	Asn	Arg	Ile	
	eu Lys .30	Gly	Ile	Asp	Phe 135	Lys	Glu	Asp	Gly	Asn 140	Ile	Leu	Gly	His	
Lys L 145	eu Glu	Tyr	Asn	Tyr 150	Asn	Ser	His	Asn	Val 155	Tyr	Ile	Met	Ala	Asp 160	

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Lys Gln Lys Asn Gly Ile Lys Val Asn Phe Lys Ile Arq His Asn Ile
Glu Asp Gly Ser Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro
Ile Gly Asp Gly Pro Val Leu Leu Pro Asp Asn His Tyr Leu Ser Thr
Gln Ser Ala Leu Ser Lys Asp Pro Asn Glu Lys Arg Asp His Met Val
                          215
Leu Leu Glu Phe Val Thr Ala Ala Gly Ile Thr His Gly Met Asp Glu
225
Leu Tyr Lys
<210> 117
<211> 732
<212> DNA
<213> Artificial Sequence
<220>
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<221> CDS
<222> (1)..(732)
<400> 117
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Met Val Val Val Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val
                                                                       48
gtc cca att ctc gtg gaa ctg gat ggc gat gtg aat ggg cac aaa ttt
                                                                       96
Val Pro Ile Leu Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe
              20
                                   25
tct gtc agc gga gag ggt gaa ggt gat gcc aca tac gga aag ctc acc
                                                                       144
Ser Val Ser Gly Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr
                               40
ctg aaa ttc atc tgc acc act gga aag ctc cct gtg cca tgg cca aca
Leu Lys Phe Ile Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr
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	50					55					60					
ctg Leu 65	gtc Val	act Thr	acc Thr	ttc Phe	tct Ser 70	tat Tyr	ggc Gly	gtg Val	cag Gln	tgc Cys 75	ttt Phe	tcc Ser	aga Arg	tac Tyr	cca Pro 80	240
														gag Glu 95		288
		_		_							_			tac Tyr	_	336
														aga Arg		384
														ggc Gly		432
_		_											_	gcc Ala	_	480
														aac Asn 175		528
gag Glu	gat Asp	gga Gly	tcc Ser 180	gtg Val	cag Gln	ctg Leu	gcc Ala	gac Asp 185	cat His	tat Tyr	caa Gln	cag Gln	aac Asn 190	act Thr	cca Pro	576
		-							-				_	tcc Ser		624
														atg Met		672
														gac Asp		720

ctg tac aag tga Leu Tyr Lys 732

<210> 118

<211> 243

<212> PRT

<213> Artificial Sequence

<400> 118

Met Val Val Val Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val 1 5 10 15

Val Pro Ile Leu Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe 20 25 30

Ser Val Ser Gly Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr 35 40 45

Leu Lys Phe Ile Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr 50 55 60

Leu Val Thr Thr Phe Ser Tyr Gly Val Gln Cys Phe Ser Arg Tyr Pro 65 70 75 80

Asp His Met Lys Gln His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly 85 90 95

Tyr Val Gln Glu Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys 100 105 110

Thr Arg Ala Glu Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile 115 120 125

Glu Leu Lys Gly Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His 130 135 140

Lys Leu Glu Tyr Asn Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp 145 150 155 160

Lys Gln Lys Asn Gly Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile $165 \\ 0.05 \\ 170 \\ 175 \\ 175$

Glu Asp Gly Ser Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro

			180					185					190			
Ile	Gly	Asp 195	Gly	Pro	Val	Leu	Leu 200	Pro	Asp	Asn	His	Tyr 205	Leu	Ser	Thr	
Gln	Ser 210	Ala	Leu	Ser	Lys	Asp 215	Pro	Asn	Glu	Lys	Arg 220	Asp	His	Met	Val	
Leu 225	Leu	Glu	Phe	Val	Thr 230	Ala	Ala	Gly	Ile	Thr 235	His	Gly	Met	Asp	Glu 240	
Leu	Tyr	Lys														
<211 <212)> 11 L> 73 2> DN 3> Ar	32 JA	icial	l Sec	quen	ce										
<220 <223		escri	iptio	on of	f Art	cifi	cial	Sequ	ience	e: Va	al(G:	TT) 50	GFP			
	> CI		(732))												
atg)> 11 gtt Val	gtt	gtt Val	gtt Val 5	gtt Val	agc Ser	aag Lys	ggc Gly	gag Glu 10	gaa Glu	ctg Leu	ttc Phe	act Thr	ggc Gly 15	gtg Val	48
gtc Val	cca Pro	att Ile	ctc Leu 20	gtg Val	gaa Glu	ctg Leu	gat Asp	ggc Gly 25	gat Asp	gtg Val	aat Asn	ggg Gly	cac His 30	aaa Lys	ttt Phe	96
tct Ser	gtc Val	agc Ser 35	gga Gly	gag Glu	ggt Gly	gaa Glu	ggt Gly 40	gat Asp	gcc Ala	aca Thr	tac Tyr	gga Gly 45	aag Lys	ctc Leu	acc Thr	144
ctg Leu	aaa Lys 50	ttc Phe	atc Ile	tgc Cys	acc Thr	act Thr 55	gga Gly	aag Lys	ctc Leu	cct Pro	gtg Val 60	cca Pro	tgg Trp	cca Pro	aca Thr	192
ctg Leu	gtc Val	act Thr	acc Thr	ttc Phe	tct Ser	tat Tyr	ggc Gly	gtg Val	cag Gln	tgc Cys	ttt Phe	tcc Ser	aga Arg	tac Tyr	cca Pro	240

65					70			75			80	
				cag Gln 85								288
				aga Arg								336
				gtc Val								384
				att Ile								432
				aac Asn								480
				ggc Gly 165								528
				gtg Val								576
				cct Pro								624
				tct Ser								672
				gtg Val								720
_	tac Tyr	_	tga									732

<210> 120

<211> 243

<212> PRT

<213> Artificial Sequence

<400> 120

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Val Pro Ile Leu Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe 20 25 30

Ser Val Ser Gly Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr 35 40 45

Leu Lys Phe Ile Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr 50 55 60

Leu Val Thr Thr Phe Ser Tyr Gly Val Gln Cys Phe Ser Arg Tyr Pro 65 70 75 80

Asp His Met Lys Gln His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly 85 90 95

Tyr Val Gln Glu Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys 100 105 110

Thr Arg Ala Glu Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile 115 120 125

Glu Leu Lys Gly Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His 130 135 140

Lys Leu Glu Tyr Asn Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp 145 150 155 160

Lys Gln Lys Asn Gly Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile
165 170 175

Glu Asp Gly Ser Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro 180 185 190

Ile Gly Asp Gly Pro Val Leu Leu Pro Asp Asn His Tyr Leu Ser Thr 195 200 205

Gln	Ser 210	Ala	Leu	Ser	Lys	Asp 215	Pro	Asn	Glu	Lys	Arg 220	Asp	His	Met	Val	
Leu 225	Leu	Glu	Phe	Val	Thr 230	Ala	Ala	Gly	Ile	Thr 235	His	Gly	Met	Asp	Glu 240	
Leu	Tyr	Lys														
<211 <212)> 12 L> 73 2> DN 3> Ar	32 NA	icia.	L Sed	quenc	ce										
<220 <223		escri	iptic	on of	f Art	cific	cial	Sequ	ıence	∋: St	op (5	TAA) 5	GFP			
)> L> CI 2> (1		(732))												
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														aaa Lys		96
tct Ser	gtc Val	agc Ser 35	gga Gly	gag Glu	ggt Gly	gaa Glu	ggt Gly 40	gat Asp	gcc Ala	aca Thr	tac Tyr	gga Gly 45	aag Lys	ctc Leu	acc Thr	144
ctg Leu	aaa Lys 50	ttc Phe	atc Ile	tgc Cys	acc Thr	act Thr 55	gga Gly	aag Lys	ctc Leu	cct Pro	gtg Val 60	cca Pro	tgg Trp	cca Pro	aca Thr	192
														tac Tyr		240

gac cat atg aag cag cat gac ttt ttc aag agc gcc atg ccc gag ggc 288

Asp	His	Met	Lys	Gln 85	His	Asp	Phe	Phe	Lys 90	Ser	Ala	Met	Pro	Glu 95	Gly	
		cag Gln														336
		gct Ala 115														384
		aag Lys														432
		gaa Glu														480
		aag Lys														528
		gga Gly														576
		gac Asp 195														624
_		gcc Ala	-			-			_	_	_	_		_	-	672
_	_	gag Glu				_	_						_	_		720
_	tac Tyr	aag Lys	tga													732

<210> 122 <211> 732

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<220> <223> Description of Artificial Sequence: Stop(TAG)5GFP	
<220> <221> CDS <222> (1)(732)	
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gtc cca att ctc gtg gaa ctg gat ggc gat gtg aat ggg cac aaa ttt 999	96
tot gto ago gga gag ggt gaa ggt gat goo aca tac gga aag oto aco Ser Val Ser Gly Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr 35 40 45	144
ctg aaa ttc atc tgc acc act gga aag ctc cct gtg cca tgg cca aca Leu Lys Phe Ile Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr 50 55 60	192
ctg gtc act acc ttc tct tat ggc gtg cag tgc ttt tcc aga tac cca 2 Leu Val Thr Thr Phe Ser Tyr Gly Val Gln Cys Phe Ser Arg Tyr Pro 65 70 75 80	240
gac cat atg aag cag cat gac ttt ttc aag agc gcc atg ccc gag ggc 2 Asp His Met Lys Gln His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly 85 90 95	288
tat gtg cag gag aga acc atc ttt ttc aaa gat gac ggg aac tac aag Tyr Val Gln Glu Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys 100 105 110	336
acc cgc gct gaa gtc aag ttc gaa ggt gac acc ctg gtg aat aga atc Thr Arg Ala Glu Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile 115 120 125	384
gag ctg aag ggc att gac ttt aag gag gat gga aac att ctc ggc cac	432

<400> 123

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Glu Leu Lys Gly Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His
aag ctg gaa tac aac tat aac too cac aat gtg tac atc atg goo gac
                                                                   480
Lys Leu Glu Tyr Asn Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp
aag caa aag aat ggc atc aag gtc aac ttc aag atc aga cac aac att
                                                                   528
Lys Gln Lys Asn Gly Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile
                                    170
gag gat gga tcc gtg cag ctg gcc gac cat tat caa cag aac act cca
                                                                   576
Glu Asp Gly Ser Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro
                                185
atc ggc gac ggc cct gtg ctc ctc cca gac aac cat tac ctg tcc acc
                                                                   624
Ile Gly Asp Gly Pro Val Leu Leu Pro Asp Asn His Tyr Leu Ser Thr
        195
                            200
cag tot goo ctg tot aaa gat coo aac gaa aag aga gac cac atg gto
                                                                   672
Gln Ser Ala Leu Ser Lys Asp Pro Asn Glu Lys Arg Asp His Met Val
    210
                        215
ctg ctg gag ttt gtg acc gct gct ggg atc aca cat ggc atg gac gag
                                                                   720
Leu Leu Glu Phe Val Thr Ala Ala Gly Ile Thr His Gly Met Asp Glu
225
                    230
                                         235
ctg tac aag tga
                                                                   732
Leu Tyr Lys
<210> 123
<211> 732
<212> DNA
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<223> Description of Artificial Sequence: Stop(TGA)5GFP
<220>
<221> CDS
<222> (1)..(732)
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														aaa Lys		96
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ctg Leu	aaa Lys 50	ttc Phe	atc Ile	tgc Cys	acc Thr	act Thr 55	gga Gly	aag Lys	ctc Leu	cct Pro	gtg Val 60	cca Pro	tgg Trp	cca Pro	aca Thr	192
ctg Leu 65	gtc Val	act Thr	acc Thr	ttc Phe	tct Ser 70	tat Tyr	ggc Gly	gtg Val	cag Gln	tgc Cys 75	ttt Phe	tcc Ser	aga Arg	tac Tyr	cca Pro 80	240
gac Asp	cat His	atg Met	aag Lys	cag Gln 85	cat His	gac Asp	ttt Phe	ttc Phe	aag Lys 90	agc Ser	gcc Ala	atg Met	ccc Pro	gag Glu 95	ggc Gly	288
tat Tyr	gtg Val	cag Gln	gag Glu 100	aga Arg	acc Thr	atc Ile	ttt Phe	ttc Phe 105	aaa Lys	gat Asp	gac Asp	ggg Gly	aac Asn 110	tac Tyr	aag Lys	336
acc Thr	cgc Arg	gct Ala 115	gaa Glu	gtc Val	aag Lys	ttc Phe	gaa Glu 120	ggt Gly	gac Asp	acc Thr	ctg Leu	gtg Val 125	aat Asn	aga Arg	atc Ile	384
gag Glu	ctg Leu 130	aag Lys	ggc Gly	att Ile	gac Asp	ttt Phe 135	aag Lys	gag Glu	gat Asp	gga Gly	aac Asn 140	att Ile	ctc Leu	ggc Gly	cac His	432
aag Lys 145	ctg Leu	gaa Glu	tac Tyr	aac Asn	tat Tyr 150	aac Asn	tcc Ser	cac His	aat Asn	gtg Val 155	tac Tyr	atc Ile	atg Met	gcc Ala	gac Asp 160	480
aag Lys	caa Gln	aag Lys	aat Asn	ggc Gly 165	atc Ile	aag Lys	gtc Val	aac Asn	ttc Phe 170	aag Lys	atc Ile	aga Arg	cac His	aac Asn 175	att Ile	528
gag	gat	gga	tcc	gtg	cag	ctg	gcc	gac	cat	tat	caa	cag	aac	act	cca	576

Glu Asp Gly	Ser Val Gl: 180		Asp His Tyr 185	Gln Gln Asn 190	
			cca gac aac Pro Asp Asn		
cag tct gcc Gln Ser Ala 210	ctg tct aa Leu Ser Ly	a gat ccc a s Asp Pro A 215	aac gaa aag Asn Glu Lys	aga gac cac Arg Asp His 220	atg gtc 672 Met Val
ctg ctg gag Leu Leu Glu 225	ttt gtg ac Phe Val Th 23	Ala Ala 🤇	ggg atc aca Gly Ile Thr 235	cat ggc atg His Gly Met	gac gag 720 Asp Glu 240
ctg tac aag Leu Tyr Lys	tga				732
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gaa ctg gat Glu Leu Asp	ggc gat gto Gly Asp Val 20	g aat ggg o . Asn Gly H	cac aaa ttt His Lys Phe 25	tct gtc agc Ser Val Ser 30	gga gag 96 Gly Glu
ggt gaa ggt Gly Glu Gly 35	gat gcc aca Asp Ala Th	a tac gga a Tyr Gly I 40	aag ctc acc Lys Leu Thr	ctg aaa ttc Leu Lys Phe 45	atc tgc 144 Ile Cys

acc Thr	act Thr 50	gga Gly	aag Lys	ctc Leu	cct Pro	gtg Val 55	cca Pro	tgg Trp	cca Pro	aca Thr	ctg Leu 60	gtc Val	act Thr	acc Thr	ttc Phe	192
	tat Tyr															240
	gac Asp															288
	atc Ile															336
	ttc Phe															384
gac Asp	ttt Phe 130	aag Lys	gag Glu	gat Asp	gga Gly	aac Asn 135	att Ile	ctc Leu	ggc Gly	cac His	aag Lys 140	ctg Leu	gaa Glu	tac Tyr	aac Asn	432
tat Tyr 145	aac Asn	tcc Ser	cac His	aat Asn	gtg Val 150	tac Tyr	atc Ile	atg Met	gcc Ala	gac Asp 155	aag Lys	caa Gln	aag Lys	aat Asn	ggc Gly 160	480
atc Ile	aag Lys	gtc Val	aac Asn	ttc Phe 165	aag Lys	atc Ile	aga Arg	cac His	aac Asn 170	att Ile	gag Glu	gat Asp	gga Gly	tcc Ser 175	gtg Val	528
cag Gln	ctg Leu	gcc Ala	gac Asp 180	cat His	tat Tyr	caa Gln	cag Gln	aac Asn 185	act Thr	cca Pro	atc Ile	ggc Gly	gac Asp 190	ggc Gly	cct Pro	576
gtg Val	ctc Leu	ctc Leu 195	cca Pro	gac Asp	aac Asn	cat His	tac Tyr 200	ctg Leu	tcc Ser	acc Thr	cag Gln	tct Ser 205	gcc Ala	ctg Leu	tct Ser	624
aaa Lys	gat Asp 210	ccc Pro	aac Asn	gaa Glu	aag Lys	aga Arg 215	gac Asp	cac His	atg Met	gtc Val	ctg Leu 220	ctg Leu	gag Glu	ttt Phe	gtg Val	672
acc	gct	gct	ggg	atc	aca	cat	ggc	atg	gac	gag	ctg	tac	aag	tga		717

Thr Ala Ala Gly Ile Thr His Gly Met Asp Glu Leu Tyr Lys 225 230 235

<210> 125

<211> 238

<212> PRT

<213> Artificial Sequence

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Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly Glu 20 25 30

Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile Cys $35 \hspace{1cm} 40 \hspace{1cm} 45$

Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr Phe 50 55 60

Ser Tyr Gly Val Gln Cys Phe Ser Arg Tyr Pro Asp His Met Lys Gln 65 70 75 80

His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu Arg \$85\$ 90 95

Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu Val

Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly Ile 115 120 125

Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr Asn 130 135 140

Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp Lys Gln Lys Asn Gly 150 150 155 160

Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile Glu Asp Gly Ser Val 165 170 175

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Val Leu Pro Asp Asn His Tyr Leu Ser Thr Gln Ser Ala Leu Ser
                            200
Lys Asp Pro Asn Glu Lys Arg Asp His Met Val Leu Leu Glu Phe Val
Thr Ala Ala Gly Ile Thr His Gly Met Asp Glu Leu Tyr Lys
                    230
<210> 126
<211> 54
<212> DNA
<213> Artificial Sequence
<220>
<223> Description of Artificial Sequence: Ala(GCA)5
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<210> 127
<211> 54
<212> DNA
<213> Artificial Sequence
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      primer
<400> 127
cggggtacca tggccgccgc cgccgccagc aagggcgagg aactqttcac tggc
                                                                   54
<210> 128
<211> 54
<212> DNA
<213> Artificial Sequence
<220>
<223> Description of Artificial Sequence: Ala(GCG)5
      primer
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<400> cggggt	128 acca tggcggcggc ggcggcg <u>agc</u> aagggcgagg aactgttcac tggc	54
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<210> :<211> :<212> :<213> :	54	
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<210> 1 <211> 3 <212> I <213> I	54	
<220> <223> I	Description of Artificial Sequence: Arg(AGG)5 primer	
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<210> 3	132	

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                                                                  54
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      primer
<400> 133
cggggtacca tgcgccgccg ccgccgcagc aagggcgagg aactgttcac tggc
                                                                  54
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<223> Description of Artificial Sequence: Arg(CGG)5
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cggggtacca tgcggcggcg gcggcggagc aagggcgagg aactgttcac tggc
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<223> Description of Artificial Sequence: arg(CGT)5
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	primer		
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<210><211><212><212><213>	54		
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<223> Description of Artificial Sequence: Asp(GAT)5
      primer
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<210> 140
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<212> DNA
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<223> Description of Artificial Sequence: Cys(TGC)5
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cggggtacca tgtgctgctg ctgctgcagc aagggcgagg aactgttcac tggc
                                                                    54
<210> 141
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<223> Description of Artificial Sequence: Cys(TGT)5
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<210> 142
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<210> 143 <211> 54 <212> DNA <213> Artificial Sequence	
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<400> 143 cggggtacca tgcagcagca gcagcag <u>agc</u> aagggcgagg aactgttcac tggc 5	4
<210> 144 <211> 54 <212> DNA <213> Artificial Sequence	
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<210> 145 <211> 54 <212> DNA <213> Artificial Sequence	
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<211> 54
<212> DNA
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<223> Description of Artificial Sequence: Gly(GGA)5
      primer
<400> 146
cggggtacca tgggaggagg aggagga<u>agc</u> aagggcgagg aactgttcac tggc
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<210> 147
<211> 54
<212> DNA
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<223> Description of Artificial Sequence: Gly(GGC)5
      primer
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cggggtacca tgggcggcgg cggcggcagc aagggcgagg aactgttcac tggc
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<210> 148
<211> 54
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<223> Description of Artificial Sequence: Gly(GGG)5
      primer
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cggggtacca tgggggggg gggggggagc aagggcgagg aactgttcac tggc
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<220> <223>	Description of Artificial Sequence: Gly(GGT)5 primer		
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<210> <211> <212> <213>	54		
<220> <223>	Description of Artificial Sequence: His(CAC)5 primer		
<400> cggggt	150 zacca tgcaccacca ccaccac <u>agc</u> aagggcgagg aactgttcac	tggc	54
<210><211><211><212><213>	54		
<220> <223>	Description of Artificial Sequence: His(CAT)5 primer		
<400> cggggt	151 acca tgcatcatca tcatcat <u>agc</u> aagggcgagg aactgttcac	tggc	54
<210><211><211><212><213>	54		
<220> <223>	Description of Artificial Sequence: Ile(ATA)5 primer		
<400> cggggt	152 acca tgataataat aataata <u>agc</u> aagggcgagg aactgttcac :	tggc	54

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<210> 153
<211> 54
<212> DNA
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<220>
<223> Description of Artificial Sequence: Ile(ATC)5
      primer
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cggggtacca tgatcatcat catcatcagc aagggcgagg aactgttcac tggc
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<212> DNA
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<223> Description of Artificial Sequence: Ile(ATT)5
      primer
<400> 154
cggggtacca tgattattat tattattagc aagggcgagg aactgttcac tggc
                                                                  54
<210> 155
<211> 54
<212> DNA
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<223> Description of Artificial Sequence: Leu(CTA)5
      primer
<400> 155
cggggtacca tgctactact actactaagc aagggcgagg aactgttcac tggc
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<210> 156
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<212> DNA
<213> Artificial Sequence
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<220> <223>	Description of Artificial Sequence: Leu(CTC)5 primer	
<400> cggggt	156 acca tgctcctcct cctcctc <u>agc</u> aagggcgagg aactgttcac tggc	54
<210><211><212><212><213>	54	
<220> <223>	Description of Artificial Sequence: Leu(CTG)5 primer	
<400> cggggt	157 cacca tgctgctgct gctgctg <u>agc</u> aagggcgagg aactgttcac tggc	54
<210><211><211><212><213>	54	
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cggggtacca tgttattatt attatta <u>agc</u> aagggcgagg aactgttcac tggc	54
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<220> <223> Description of Artificial Sequence: Lys(AAA)5 primer	
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<210> 162 <211> 54 <212> DNA <213> Artificial Sequence	
<220> <223> Description of Artificial Sequence: Lys(AAG)5 primer	
<400> 162 cggggtacca tgaagaagaa gaagaagagc aagggcgagg aactgttcac tggc	54
<210> 163 <211> 54 <212> DNA	

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<223> Description of Artificial Sequence: Phe(CTT)5
      primer
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cggggtacca tgcttcttct tcttcttagc aagggcgagg aactgttcac tggc
<210> 164
<211> 54
<212> DNA
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<220>
<223> Description of Artificial Sequence: Phe(TTC)5
      primer
<400> 164
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<210> 165
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<212> DNA
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<223> Description of Artificial Sequence: Pro(CCC)5
      primer
<400> 165
cggggtacca tgccccccc ccccccagc aagggcgagg aactgttcac tggc
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<210> 166
<211> 54
<212> DNA
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<223> Description of Artificial Sequence: Pro(CCG)5
      primer
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<400> cggggt	166 tacca tgeegeegee geegeeg <u>age</u> aagggegagg aactgtteae tgge	c 54
<210><211><211><212><213>	54	
<220> <223>	Description of Artificial Sequence: Pro(CCT)5 primer	
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<210><211><211><212><213>	54	
<220> <223>	Description of Artificial Sequence: Pro(CGA)5 primer	
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<210><211><212><213>	54	
<220> <223>	Description of Artificial Sequence: Ser(AGC)5 primer	
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<210> <211>		

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<212> DNA
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<223> Description of Artificial Sequence: Ser(AGT)5
      primer
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<210> 171
<211> 54
<212> DNA
<213> Artificial Sequence
<220>
<223> Description of Artificial Sequence: Ser(TCA)5
      primer
<400> 171
cggggtacca tgtcatcatc atcatca<u>agc</u> aagggcgagg aactgttcac tggc
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<210> 1726
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<212> DNA
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      primer
<400> 172
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                                                                    54
<210> 173
<211> 54
<212> DNA
<213> Artificial Sequence
<220>
<223> Description of Artificial Sequence: Ser(TCG)5
      primer
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<210><211><212><212><213>	54		
	Description of Artificial Sequence: Ser(TCT)5 primer		
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<210><211><211><212><213>	54		
	Description of Artificial Sequence: Thr(ACA)5 primer		
<400> cggggt	175 acca tgacaacaac aacaaca <u>agc</u> aagggcgagg aactgttcac	tggc	54
<210><211><211><212><213>	54		
	Description of Artificial Sequence: Thr(ACC)5		
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<210>	177		

<211> <212> <213>		
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<400> cggggt	177 tacca tgacgacgac gacgacg <u>agc</u> aagggcgagg aactgttcac tggc	54
<210><211><211><212><213>	54	
<220> <223>	Description of Artificial Sequence: Thr(ACT)5 primer	
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<210><211><211><212><213>	54	
<220> <223>	Description of Artificial Sequence: Trp(TGG)5 primer	
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<210><211><212><212><213>	54	
<220>	Description of Artificial Sequence: Tvr(TAT)5	

	primer	
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<210><211><211><212><213>	54	
<220> <223>	Description of Artificial Sequence: Val(GTA)5 primer	
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<210><211><211><212><213>	54	
<220> <223>	Description of Artificial Sequence: Val(GTC)5 primer	
<400> cggggt	182 tacca tggtcgtcgt cgtcgtc <u>agc</u> aagggcgagg aactgttcac tggc	54
<210><211><211><212><213>	54	
<220> <223>	Description of Artificial Sequence: Val(GTG)5 primer	
<400>	183 tacca tggtggtggt ggtggtg <u>agc</u> aagggcgagg aactgttcac tggc	54

<210><211><211><212><213>	54	
<220> <223>	Description of Artificial Sequence: Val(GTT)5 primer	
<400>	184 tacca tggttgttgt tgttgtt <u>agc</u> aagggcgagg aactgttcac tggc	54
<210> <211> <212> <213>	33	
<220> <223>	Description of Artificial Sequence: 3' oligonucleotide common primer	
<400> ccgga	185 attc <u>t ca</u> cttgtaca ggtggtccat gcc	33